

; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-902-188A-7

Query Match 96.5%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDELGEFNFQKGTIRTKYGTNRQLQAQVAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Db 61 YDYLDELGEFNFQKGTIRTKYGTNRQLQAQVAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTIETAWTKFDPPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTIETAWTKFDPPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Qy 181 RDKGKAWDEVDTEGNGYDYLMTADIDMDHPEVNNELRNWGVYTNLTGLDGFRIIDAVKH 240
Db 181 RDKGKAWDEVDTEGNGYDYLMTADIDMDHPEVNNELRNWGVYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLNKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLNKTNWHSVDFVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARQKAYGRNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARQKAYGRNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGWNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGWNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 11
US-09-925-576C-13
; Sequence 13, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjørn Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 1004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: bacillus sp. 707
US-09-925-576C-13

Query Match 96.5%; Score 2613; DB 10; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDELGEFNFQKGTIRTKYGTNRQLQAQVAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Db 61 YDYLDELGEFNFQKGTIRTKYGTNRQLQAQVAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTIETAWTKFDPPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTIETAWTKFDPPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Qy 181 RDKGKAWDEVDTEGNGYDYLMTADIDMDHPEVNNELRNWGVYTNLTGLDGFRIIDAVKH 240
Db 181 RDKGKAWDEVDTEGNGYDYLMTADIDMDHPEVNNELRNWGVYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLNKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLNKTNWHSVDFVPLHYNLYNA 300
Qy 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDQSPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARQKAYGRNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARQKAYGRNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGWNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKMWFGVGRNKAGQVWTDITGNRAGTGTINADGWNFVSGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 12
US-10-665-667-6
; Sequence 6, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjørn
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Søren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-6

Query Match 96.5%; Score 2613; DB 12; Length 485;
Best Local Similarity 95.5%; Pred. No. 7e-234;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDYLDELGEFNFQKGTIRTKYGTNRQLQAQVAVTSLKNNGIQVYGVVMMHKGADATEMVRV 120

Db 61 YDLGFEFQKGVTRTKYGRSLQAAVTSKXNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYTTIEAWTKFDPGRCNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTRFDPGRCNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
QY 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
Db 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATKQMFVAEAEFKNLGAENYLNKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATKQMFVAEAEFKNLGAENYLNKTNHNSVDFVPLHYNLYNA 300
QY 301 SKSGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYGYGIPTHGVPAKMSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGIPTHGVPAKMSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
Db 421 HPNSGLATIMSDGAGGKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 13

US-10-025-648-7

; Sequence 7, Application US/10025648

; Publication No. US20030064908A1

; GENERAL INFORMATION:

; APPLICANT: Bisgard-Frantzen, Henrik

; Svendsen, Allan

; Borchert, Torben Vedel

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Novo Nordisk of North America, Inc.

; STREET: 405 Lexington Avenue, Suite 6400

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/025,648

; FILING DATE: 19-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/600,656

; FILING DATE: 13-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Lambiris, Elias J.

; REGISTRATION NUMBER: 33,728

; REFERENCE/DOCKET NUMBER: 4318.204-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 867 0123

; TELEFAX: 212 867 0298

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 485 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-025-648-7

Query Match 96.5%; Score 2613; DB 12; Length 485;

Best Local Similarity 95.5%; Pred. No. 7e-234;

Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFPEWYLPNDGNHNRSLSDASNLKDGISAVTIPPAWKASQNDVGGA 60

Db 1 HHNGTGTMMQYFPEWYLPNDGNHNRSLSDASNLKDGISAVTIPPAWKASQNDVGGA 60

QY 61 YDLGFEFQKGVTRTKYGRSLQAAVTSKXNGIQVYGDVVMNHKGGADATEMVRV 120

Db 61 YDLGFEFQKGVTRTKYGRSLQAAVTSKXNGIQVYGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNRNQEVSGEYTTIEAWTKFDPGRCNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

Db 121 EVNPNRNQEVSGEYTTIEAWTRFDPGRCNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180

QY 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240

Db 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNKGWVYTNLTGLDGFPRIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATKQMFVAEAEFKNLGAENYLNKTNHNSVDFVPLHYNLYNA 300

Db 241 IKYSFTRDWINHVRSAATKQMFVAEAEFKNLGAENYLNKTNHNSVDFVPLHYNLYNA 300

QY 301 SKSGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360

Db 301 SKSGNYDMRQIFNGTVVQRHPMAVTFVNDHDSQPEALESFVEEWFKPLAYALTITRE 360

QY 361 QGYPSVFYGYGIPTHGVPAKMSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420

Db 361 QGYPSVFYGYGIPTHGVPAKMSKIDPILFARQKAYAGQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480

Db 421 HPNSGLATIMSDGAGGKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFVSGSVS 480

QY 481 IWVWK 485

Db 481 IWVWK 485

RESULT 14

US-10-327-837-6

; Sequence 6, Application US/10327837

; Publication No. US20030211958A1

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan

; APPLICANT: Borchert, Torben Vedel

; APPLICANT: Bisgard-Frantzen Henrik

; APPLICANT: Outtrup, Helle

; APPLICANT: Nielsen, Bjarne Ronfeldt

; APPLICANT: Nielsen, Vibeke Skovgaard

; APPLICANT: Hoeck, Lisbeth Hedegaard

; TITLE OF INVENTION: Novel - Amylase And -Amylase Mutants

; FILE REFERENCE: 5276.400-US

; CURRENT APPLICATION NUMBER: US/10/327,837

; PRIORITY FILING DATE: 2002-12-23

; PRIOR APPLICATION NUMBER: US/09/290,734

; PRIOR FILING DATE: 1999-04-13

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: Fast-SEQ for Windows Version 3.0

; SEQ ID NO 6

; LENGTH: 485

; TYPE: PRT

; ORGANISM: Bacillus sp.

; US-10-327-837-6

Query Match 96.5%; Score 2613; DB 12; Length 485;

Best Local Similarity 95.5%; Pred. No. 7e-234; Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;									
Qy	1	HNGTNGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWIPPAWKASQNDVGYGA	60						
Db	1	HNGTNGTMMQYFEWYLPNDGNHNRRLSDASNLKKGITAVWIPPAWKASQNDVGYGA	60						
Qy	61	YDLYDLGEFNQKGTIRTKYTRNQLQAANALXSGIQVYGDVVMNHKGGADATEMVRV	120						
Db	61	YDLYDLGEFNQKGTIRTKYTRNQLQAATSLKNGIQVYGDVVMNHKGGADATEMVRV	120						
Qy	121	EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF	180						
Db	121	EVNPNRNQEVSGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNRIYKF	180						
Qy	181	RGDGKAWDEVDTEGNGYDLYMADIMDHPVNNELRWGVWYTTTLGLDGFRIIDAVKH	240						
Db	181	RGDGKAWDEVDTEGNGYDLYMADIMDHPVNNELRWGVWYTTTLGLDGFRIIDAVKH	240						
Qy	241	IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA	300						
Qy	301	SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEEALESFVEEWFKPLAYALTLTRE	360						
Db	301	SKSGGNYDMRNIENGTVVQRHPSHAVTFVDNHDSPPEEALESFVEEWFKPLAYALTLTRE	360						
Qy	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420						
Db	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYQKNDYLDHNNIIGWTREGNTA	420						
Qy	421	HPNSGLATTIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS	480						
Db	421	HPNSGLATTIMSDGAGGSKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480						
Qy	481	IWNK 485							
Db	481	IWNK 485							
Search completed: October 7, 2004, 00:57:32 Job time : 55.4478 secs									

Qy	121	EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF	180						
Db	121	EVNPNRNQEVSGEYTIETAWTRDFPGRGNTHSFKRWYHFDGVWDQSRRLNRIYKF	180						
Qy	181	RGDGKAWDEVDTEGNGYDLYMADIMDHPVNNELRWGVWYTTTLGLDGFRIIDAVKH	240						
Db	181	RGDGKAWDEVDTEGNGYDLYMADIMDHPVNNELRWGVWYTTTLGLDGFRIIDAVKH	240						
Qy	241	IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA	300						
Db	241	IKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA	300						
Qy	301	SKSGGNYDMRQIFNGTVVQRHPMHAVTFVDNHDSPPEEALESFVEEWFKPLAYALTLTRE	360						
Db	301	SKSGGNYDMRNIENGTVVQRHPSHAVTFVDNHDSPPEEALESFVEEWFKPLAYALTLTRE	360						
Qy	361	QGYPSVFGDYGIPTHGVPAMKSKIDPILFARQKYAYGRONDYLDHNNIIGWTREGNTA	420						
Db	361	QGYPSVFGDYGIPTHGVPAMRSKIDPILFARQKYAYQKNDYLDHNNIIGWTREGNTA	420						
Qy	421	HPNSGLATTIMSDGAGGNKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS	480						
Db	421	HPNSGLATTIMSDGAGGSKWMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS	480						
Qy	481	IWNK 485							
Db	481	IWNK 485							

RESULT 15 US-10-477-725-13 ; Sequence 13, Application US/10477725 ; Publication No. US20040096952A1 ; GENERAL INFORMATION: ; APPLICANT: NOVZYMES A/S ; APPLICANT: Svendsen, Allan ; APPLICANT: Andersen, Carsten ; APPLICANT: Thisted, Thomas ; APPLICANT: von der Osten, Claus ; TITLE OF INVENTION: Alpha-amylase variant with altered properties ; FILE REFERENCE: 10182.204-US ; CURRENT APPLICATION NUMBER: US/10/477, 725 ; CURRENT FILING DATE: 2003-11-14 ; NUMBER OF SEQ ID NOS: 13 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 13 ; LENGTH: 485 ; TYPE: PRT ; ORGANISM: Bacillus 707 US-10-477-725-13									
Query Match 96.5%; Score 2613; DB 16; Length 485; Best Local Similarity 95.5%; Pred. No. 7e-234; Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;									
Qy	1	HNGTNGTMMQYFEWYLPNDGNHNRRLSDASNLKKGISAVWIPPAWKASQNDVGYGA	60						
Db	1	HNGTNGTMMQYFEWYLPNDGNHNRRLSDASNLKKGITAVWIPPAWKASQNDVGYGA	60						
Qy	61	YDLYDLGEFNQKGTIRTKYTRNQLQAANALXSGIQVYGDVVMNHKGGADATEMVRV	120						
Db	61	YDLYDLGEFNQKGTIRTKYTRNQLQAATSLKNGIQVYGDVVMNHKGGADATEMVRV	120						

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-13
Perfect score: 2703
Sequence: 1 HHNGTNGTMMQYPEWYLPND.....ADGNGFNVSGSVSIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2703	100.0	485	2 AAW12956	AAW12956 Alpha-amy
2	2703	100.0	485	2 AAY15420	Aay15420 Termamyl-
3	2703	100.0	485	2 AAY07386	Aay07386 Wild type
4	2703	100.0	485	3 AAY99607	Aay99607 Bacillus
5	2703	100.0	485	5 ABB06939	Abb06939 Bacillus
6	2703	100.0	485	5 AAU12155	Aau12155 Bacillus
7	2703	100.0	485	5 AAB47856	Aab47856 Bacillus
8	2703	100.0	485	5 ABB76592	Abb76592 Termamyl-
9	2613	96.7	485	3 AAY97812	Aay97812 Bacillus
10	2613	96.7	485	4 AAB29260	Aab29260 Bacillus
11	2613	96.7	485	4 AAB29261	Aab29261 Bacillus
12	2613	96.7	485	5 ABB06938	Abb06938 Bacillus
13	2613	96.7	485	5 AAU12154	Aau12154 Bacillus
14	2613	96.7	485	5 AAB47855	Aab47855 Bacillus
15	2613	96.7	485	5 ABB76591	Abb76591 Termamyl-
16	2580	95.4	480	4 ABB00046	Abb00046 AA560 SEQ
17	2551	94.4	516	5 ABB08773	Abb08773 Bacillus
18	2492.5	92.2	519	4 AAE09762	Aae09762 Bacillus
19	2492.5	92.2	519	4 AAE09763	Aae09763 Bacillus
20	2484.5	91.9	519	4 AAE09767	Aae09767 Bacillus
21	2483.5	91.9	519	4 AAE09764	Aae09764 Bacillus
22	2449	90.6	485	2 AAW12110	AAW12110 Alpha-amy
23	2442	90.3	485	2 AAW12144	AAW12144 Alpha-amy
24	2442	90.3	485	2 AAW12109	AAW12109 Alpha-amy
25	2440	90.3	485	2 AAW31499	AAW31499 Bacillus

ALIGNMENTS

RESULT 1

AAW12956

ID AAW12956 standard; protein; 485 AA.

AC AAW12956;

XX 16-OCT-2003 (revised)

DT 07-APR-1997 (first entry)

XX Alpha-amyase.

XX Alpha-amyase; detergent; thermal stability; oxidation stability; enzyme;

KW calcium ion dependency; alpha-amyolytic activity; washing composition;

KW textile desizing; papermaking; beer-making; ethanol production;

KW sweetener.

XX Bacillus sp; #707.

XX WO9623873-A1.

XX 08-AUG-1996.

XX 05-FEB-1996; 96WO-DK000056.

XX 03-FEB-1995; 95DK-00000126.

XX 29-MAR-1995; 95DK-00000336.

XX 29-SEP-1995; 95DK-00001097.

XX 06-OCT-1995; 95DK-00001121.

XX (NOVO) NOVO-NORDISK AS.

XX Bisgard-Frantzen H, Svendsen A, Borchert T;

XX WPI; 1996-371423/37.

XX Alpha-amyase variants - with improved thermal and oxidation stability and reduced calcium ion dependency.

XX Disclosure; Page 91-93; 11pp; English.

XX AAW12955, AAW12956, AAR81835 and AAR81836 represent the parent alpha-amyases used to create the variants of the invention (such as AAW12098-w12131). This sequence represents the alpha-amyase from Bacillus sp. #707. The variants of the invention were created using site directed, or random, mutagenesis of the DNA sequences encoding these parent alpha-amyases. The variants of the invention can have improved thermal stability (such as at temperatures in the range of 40-70 degrees Celcius), and/or oxidation stability, and/or reduced calcium ion

CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. The variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate. The variants can be
 CC used in detergent and washing compositions, and for textile desizing. The
 CC alpha-amylase variants can also be used in papermaking and beer-making
 CC processes. The variants of the invention can also be used in the
 CC production of sweeteners and ethanol from starch. (Updated on 16-OCT-2003
 CC to standardise OS field)
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 5.3e-219;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
 DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
 QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
 DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
 QY 121 EVNPNRNQEVGTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
 DB 121 EVNPNRNQEVGTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
 QY 181 RGHGKAWDWEVDTEGNYDLYMADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
 DB 181 RGHGKAWDWEVDTEGNYDLYMADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
 QY 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLOKTNWNHNSVDVPLHYNLYNA 300
 DB 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLOKTNWNHNSVDVPLHYNLYNA 300
 QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 QY 361 QGYPSVFGDYGIPTGHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 DB 361 QGYPSVFGDYGIPTGHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
 DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
 QY 481 IWVNK 485
 DB 481 IWVNK 485

RESULT 2
 AAY15420
 ID AAY15420 standard; protein; 485 AA.
 XX
 AC AAY15420;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Termamyl-like alpha-amylase protein.
 XX
 KW Termamyl-like; alpha-amylase; variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KW saccharification process.
 XX
 OS Bacillus sp.
 XX
 PN WO9923211-A1.
 XX
 PD 14-MAY-1999.

XX 30-OCT-1998; 98WO-DK000471.
 PF
 XX 30-OCT-1997; 97DK-00001240.
 PR
 PR 14-JUL-1998; 98DK-00000936.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nissen TL;
 PI Kjaerulff S;
 XX
 XX WPI; 1999-326987/27.
 DR
 XX
 PT New Termamyl-like alpha-amylase variants.
 XX
 PS Claim 38; Page 86-87; 115pp; English.
 XX
 CC The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T141, K142, F143,
 CC D144, F145, P146, G147, R148, G149, Q174, R181, G182, D183, G184, K185,
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, E346, K385, G456, N457, K458, G459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 5.3e-219;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
 DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
 QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
 DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
 QY 121 EVNPNRNQEVGTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
 DB 121 EVNPNRNQEVGTGEYTTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
 QY 181 RGHGKAWDWEVDTEGNYDLYMADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
 DB 181 RGHGKAWDWEVDTEGNYDLYMADIDMDHPEVNNELRNWGVWYTTNTGLDGFRIIDAVKH 240
 QY 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLOKTNWNHNSVDVPLHYNLYNA 300
 DB 241 IKYSFTRDWINHVRSAATGKMFVAEFKNDLGAENYLOKTNWNHNSVDVPLHYNLYNA 300
 QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
 QY 361 QGYPSVFGDYGIPTGHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 DB 361 QGYPSVFGDYGIPTGHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
 QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
 DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
 QY 481 IWVNK 485
 DB 481 IWVNK 485

```
RESULT 3
AA07386
ID AA07386 standard; protein; 485 AA.
XX
AC AA07386;
XX
XX 16-JUL-1999 (first entry)
DE
DE Wild type Termamyl (RTM)-like alpha-amylase protein #6.
XX
XX Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
KW dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
KW ethanol.
XX
XX Bacillus sp.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 181..184
FT /note= "optionally 1, 2, 3 or all residues are deleted"
FT Misc-difference 195
FT /note= "optionally altered to any amino acid except an
FT Asn residue"
FT Misc-difference 206
FT /note= "optionally altered to any amino acid except an
FT Ile residue"
FT Misc-difference 212
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 216
FT /note= "optionally altered to any amino acid except a Glu
FT residue"
FT Misc-difference 269
FT /note= "optionally altered to any amino acid except a Lys
FT residue"
XX
XX W09919467-A1.
PN
XX
XX 22-APR-1999.
PD
XX
XX 13-OCT-1998; 98WO-DK000444.
PF
XX
XX 13-OCT-1997; 97DK-00001172.
PR
XX
XX (NOVO ) NOVO-NORDISK AS.
PA
XX
XX Svendsen A, Borchert TV, Bisgard-Prantzen H;
PI
XX
XX WPI; 1999-277632/23.
DR
XX
XX Variant alpha-amylases - useful as detergents or for textile desizing or
XX starch liquefaction.
PT
XX
XX Claim 1; Page 70-72; 93pp; English.
PS
XX
XX This sequence represents the parent sequence for new variants of a parent
XX Termamyl-like alpha-amylase with alpha-amylase activity. The variants
XX comprise mutations in 2-6 regions/positions relative to an alpha-amylase
XX from either of two Bacillus species in W09526397, B. stearothermophilus,
XX B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
XX amylase variants are detergent additives for use in detergents for
XX dishwashing, manual or automatic laundry. The variants can also be used
XX for textile desizing or starch liquefaction (e.g. for production of
XX sweeteners or ethanol)
XX
XX Sequence 485 AA;
SQ
Query Match. 100.0%; Score 2703; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HHNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGCGA 60
|||||
```

CC isolated from a Bacillus genomic DNA library. A variant may contain
CC mutations in one or more solvent exposed amino acid residues to increase
CC the overall hydrophobicity of the enzyme or the overall number of methyl
CC groups in the side chains of exposed residues may be increased. The
CC mutations can be incorporated by site-directed mutagenesis or by random
CC mutagenesis. As a result of their increased stability, the variants are
CC suitable for the industrial processing of starch, i.e. starch
CC liquefaction and saccharification. They may also be useful for washing,
CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
CC partial amino acid sequences derived from two or more alpha-amylases have
CC also been created in order to increase enzyme stability
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
DB 61 YLDYDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
QY 121 EVNPNRNNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDMQSRRLNNRIYKF 180
DB 121 EVNPNRNNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDMQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRWNGVYTTNLGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRWNGVYTTNLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLQKTNNHNSVFDVPLHLYNLA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLQKTNNHNSVFDVPLHLYNLA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTRGNTA 420
QY 481 IWVKN 485
DB 481 IWVKN 485

RESULT 5
ABB06939
ID ABB06939 standard; protein; 485 AA.
XX
AC ABB06939;
XX
DT 19-JUN-2002 (first entry)
XX Bacillus termamyl-like alpha-amylase protein SEQ ID NO:13.
DE
XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
KW washing; sweetener; ethanol; starch.
XX
OS Bacillus sp.
XX
PN WO200166712-A2.
XX

PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-DK0000144.
XX
PR 08-MAR-2000; 2000DK-00000376.
PR 15-MAR-2000; 2000US-0189857P.
PR 23-FEB-2001; 2001DK-00000303.
PR 26-FEB-2001; 2001US-0271382P.
XX
PA (NOVO) NOVOZYMES AS.
XX
XX Andersen C, Borchert TV, Nielsen BR;
PI WPI; 2002-239612/29.
XX
DR
XX
PT Novel variant of parent termamyl-like alpha-amylase useful as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
PS Claim 8; Page 150-151; 153pp; English.
XX
CC The present invention describes a variant of a parent termamyl-like alpha
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
CC positions of a group of 31 possible amino acid positions. The alteration
CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
CC Gly186, Trp189, Asn195, His202, Tyr298, Asn299, Lys302, Asn303, Asn306,
CC Arg310, Asn314, Asn320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
CC washing and/or dishwashing, textile desizing, and starch liquefaction.
CC (I) is useful as a component in hard surface cleaning detergent
CC composition, and for producing sweeteners and ethanol from starch. (I)
CC has altered solubility, preferably increased solubility, in particular
CC under washing, dish washing or hard surface cleaning conditions. The
CC present sequence represents a Bacillus termamyl-like alpha-amylase which
CC is used in the exemplification of the present invention
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
DB 61 YLDYDLGEFNQKGTVRTKYGTSQLOAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
QY 121 EVNPNRNNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDMQSRRLNNRIYKF 180
DB 121 EVNPNRNNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVDMQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRWNGVYTTNLGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDLYMAYADIMDHPVNNELRWNGVYTTNLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLQKTNNHNSVFDVPLHLYNLA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLQKTNNHNSVFDVPLHLYNLA 300
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQRHPSHAFTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMRSKIDPILAEARQKAYGKQNDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFFVGRNKGQVWSDITGNRTGTVTINADGWNFVSGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFFVGRNKGQVWSDITGNRTGTVTINADGWNFVSGSVS 480


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QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 6
AAU12155
ID AAU12155 standard; protein; 485 AA.
AC AAU12155;
XX
DT 09-APR-2002 (first entry)
DE Bacillus TERMAMYL-like alpha-amylase 707.
XX
KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
KW amylopectin; limit dextrin; NOVAMYL; 707.
XX
OS Bacillus sp.
XX
PN WO2001188107-A2.
XX
PD 22-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-DK000323.
XX
PR 12-MAY-2000; 2000DK-00000779.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Svendsen A, Jorgensen CT, Nielsen BR;
XX
DR WPI; 2002-106123/14.
XX
PT New variant of parent Termamyl-like alpha-amylase for use as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
PS Claim 5; Page 81-83; 84pp; English.
XX
CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase
CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
CC or at position 234, where the variant has alpha-amylase activity and each
CC position corresponds to a position of a parent Termamyl-like alpha-
CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
CC of 483 amino acids, given in specification. The variant alpha- amylase, a
CC detergent additive comprising the variant or a detergent composition
CC comprising the variant, is useful for washing and/or dishwashing or
CC textile desizing. The alpha-amylase is useful for starch liquefaction or
CC ethanol production and as a component in a hard surface cleaning
CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1,6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
CC natural variant of the TERMAMYL alpha-amylase, 707
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTWQYFEWYLPNDGNHNRLNSDASNLKSGITAVWTPPAWKASQNDVGYGA 60
DB 1 HNGTGTWQYFEWYLPNDGNHNRLNSDASNLKSGITAVWTPPAWKASQNDVGYGA 60
QY 61 YLDYDLGEFNGKQVTRTKYGRSLOQAQVTSKXNGIQVYGDVVMNHKGADATEMVRV 120
DB 61 YLDYDLGEFNGKQVTRTKYGRSLOQAQVTSKXNGIQVYGDVVMNHKGADATEMVRV 120

RESULT 7
AAB47856
ID AAB47856 standard; protein; 485 AA.
XX
AC AAB47856;
XX
DT 02-APR-2002 (first entry)
DE Bacillus alpha amylase 707.
XX
KW Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
KW cured meat; fermented meat; spice.
XX
OS Bacillus sp.
XX
PN WO200196537-A2.
XX
PD 20-DEC-2001.
XX
PR 13-JUN-2001; 2001WO-DK000404.
XX
PR 14-JUN-2000; 2000DK-00000917.
XX
PR 20-JUN-2000; 2000US-0212852P.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Nielsen BR, Weibye M;
XX
DR WPI; 2002-098064/13.
XX
PT New modified alpha-amylase derived from the genus Bacillus and/or is a
PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
PT maltodextrin or glucose syrup.
XX
PS Claim 5; Page 44-46; 47pp; English.
XX
CC The sequences given in AAB47850-56 show modified alpha-amylases derived
CC from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
CC amylase and they have been pre-oxidized. The alpha amylase is useful for
CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
CC oxidized alpha-amylase until a product with a DE between 5-45 has been
CC provided and/or until a product with a molecular weight of between 5-30

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CC kda has been provided. The product comprises a maltodextrin with a DE of
CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
CC where the glucose syrup is useful as an ingredient in food, feed or
CC pharmaceuticals. Glucose syrup is useful in confectionery such as
CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
CC dairy and ice cream such as coffee whiteners, conventional foods such as
CC salad dressings, and food ingredients and preparations such as cured
CC meat, fermented meat, spices and seasoning encapsulated flavours
XX
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLIDLGEFNGKGTVRTKYGTSQLOAAVTSLNKNGIQYGVVNMHKGADATEMVRV 120
DB 61 YDLIDLGEFNGKGTVRTKYGTSQLOAAVTSLNKNGIQYGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDYADIMDHPPEVNNELRNWGVYNTLGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDYADIMDHPPEVNNELRNWGVYNTLGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSGATGKNMFAVAFWKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGATGKNMFAVAFWKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDPILFARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDPILFARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485

RESULT 8
ABB76592
ID ABB76592 standard; protein; 485 AA.
XX
XX ABB76592;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Termamyl-like-alpha-amylase #7.
DE
XX
KW Termamyl; alpha amylase; starch liquefaction; ethanol production;
KW textile desizing; detergent; enzyme.
XX
XX Bacillus sp.
OS
XX
XX WC200210355-A2.
PN
XX
XX 07-FEB-2002.
PD
XX
XX 12-JUL-2001; 2001WO-DK000488.
PF

XX
PR 01-AUG-2000; 2000DK-00001160.
PR 12-SEP-2000; 2000DK-00001354.
PR 10-NOV-2000; 2000DK-00001687.
PR 26-APR-2001; 2001DK-00000655.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Thisted T, Kjaerulff S, Andersen C, Fugleang CC;
PI
XX
XX WPI; 2002-280633/32.
DR
XX
XX Variant of parent Termamyl-like alpha amylase, useful in detergent
PT compositions, for starch liquefaction, ethanol production, washing and/or
PT dish washing, and textile desizing.
PT
XX
PS Claim 8; Page 76-78; 90pp; English.
XX
XX This invention relates to variants of a parent Termamyl-like alpha-
CC amylases. These are used for starch liquefaction, ethanol production,
CC detergent, and textile desizing. The amylases have altered stability,
CC particularly at high temperatures from 70-120plusoC and low pH in the
CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
CC amylase
XX
XX Sequence 485 AA;
SQ
Query Match 100.0%; Score 2703; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.3e-219;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLIDLGEFNGKGTVRTKYGTSQLOAAVTSLNKNGIQYGVVNMHKGADATEMVRV 120
DB 61 YDLIDLGEFNGKGTVRTKYGTSQLOAAVTSLNKNGIQYGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYITIAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDYADIMDHPPEVNNELRNWGVYNTLGLDGFRI DAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDYADIMDHPPEVNNELRNWGVYNTLGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSGATGKNMFAVAFWKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGATGKNMFAVAFWKNDLGAENYLOKTNWNHVSFVDFPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDPILFARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPAMRSKIDPILFARQKYAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485
RESULT 9
AAY97812
ID AAY97812 standard; protein; 485 AA.
XX
XX AAY97812;
AC

```

XX 12-SEP-2003 (revised)
DT 21-AUG-2000 (first entry)
XX
DE Bacillus alkaline alpha-amylase AA560.
XX
KW Alkaline alpha-amylase; AA560; immunogenicity; allergenicity;
KW industrial product; pharmaceutical; hypoallergenic.
XX
OS Bacillus sp; 'DSM12649'.
XX
XX W0200022103-A1.
XX
PD 20-APR-2000.
XX
XX 12-OCT-1999; 99WO-DK000542.
XX
XX 13-OCT-1998; 98DK-00001301.
PR 04-OCT-1999; 99DK-00001418.
XX
XX (NOVO ) NOVO-NORDISK AS.
XX
XX Olsen AA, Von Der Osten C, Andersen KV, Ernst S, Roggen EL;
XX
XX WPI; 2000-329163/28.
DR N-PSDB; AAA30783.
XX
XX New modified polypeptides having an attached polymer for reducing immune
XX responses, useful in e.g. detergents, cleaning products, skin care
XX products, food or feed products, textile products or pharmaceuticals.
XX
XX Example 4; Page 102-105; 108pp; English.
XX
XX The invention relates to proteins with reduced immunogenicity, having one
XX or more modified amino acids, where the alpha-carbon atoms of the amino
XX acids are located less than 15 Angstroms from a ligand bound to the
XX protein. The modification may entail substitution of the endogenous
XX residue for a non-endogenous residue and/or attachment of polymeric
XX molecules such as carbohydrates or branched polyethylene glycols to the
XX amino acid residues. The residue to be modified is identified from the 3-
XX dimensional structure of the protein determined, for example, by X-ray
XX crystallography or NMR. A wide variety of enzymes may be modified
XX according to the invention, including proteases (especially subtilisins),
XX carbohydrases (such as amylase), isomerases, transferases and
XX oxidoreductases. The modified proteins of the invention may be used for
XX reducing the allergenicity of industrial products (i.e., those which are
XX not intended to enter the circulatory system. The proteins may be used in
XX cleaning agents (such as laundry products, dish-washing products or hard
XX surface cleaning products), skin-care products, textile treatment
XX products (e.g., bleaching agents) and food products. The modified
XX polypeptides can also be used for reducing the immunogenicity of
XX pharmaceuticals. The modified proteins have reduced immunogenicity or
XX allergenicity while maintaining a high percentage of activity. The
XX present sequence represents an alkaline alpha-amylase, AA560, from
XX Bacillus DSM 12649, which may be modified according to the invention.
XX (Updated on 12-SEP-2003 to standardise OS field)
XX
XX Sequence 485 AA;
XX
Query Match 96.7%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPDNGNHNRLNSDASNLKSGITAVIIPPAWKGSQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPDNGNHNRLNSDASNLKSGISAVIIPPAWKGSQNDVGYGA 60
QY 61 YDLYDLGEFNQKGVTRTKYGRSLOQAATVTSKNGKIQVYGDVVMNKHGGADATEMVRAY 120
DB 61 YDLYDLGEFNQKGVTRTKYGRNLOQAATVTSKNGKIQVYGDVVMNKHGGADATEMVRAY 120
QY 121 EVNPNRNEQVSGEYTTIEAWTKFDPGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNEQVSGEYTTIEAWTKFDPGRGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGCHKAWDEVDVTENGNDYLYMAYADIOMDHPVNVNELRNWGVWYNTTILGLDGFRIIDAVKH 240
DB 181 RGCHKAWDEVDVTENGNDYLYMAYADIOMDHPVNVNELRNWGVWYNTTILGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAIEYLOKTNWNHVSFVDFPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAIEYLOKTNWNHVSFVDFPLHYNLYNA 300
QY 301 SKSGNVDNRNI FNGTVVQRHPSHAVTFVDVNDHSDQPEALESFVEEFKPLAYALTITRE 360
DB 301 SKSGNVDNRNI FNGTVVQRHPSHAVTFVDVNDHSDQPEALESFVEEFKPLAYALTITRE 360
QY 361 QGYPVSFVGDYVGIPTHGVPAMRSKIDIPILKAROKYAGKONDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFVGDYVGIPTHGVPAMRSKIDIPILKAROKYAGKONDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFEVGRNKGQVMSDITGNRTGTVTINADCGNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFEVGRNKGQVMSDITGNRTGTVTINADCGNFSVNGGSVS 480
QY 481 IWVKNK 485
DB 481 IWVKNK 485
XX
XX RESULT 10
XX AAB29260
XX ID AAB29260 standard; protein; 485 AA.
XX
XX AC AAB29260;
XX
XX DT 07-FEB-2001 (first entry)
XX
XX DE Bacillus sp. alpha-amylase #1.
XX
XX KW Alpha-amylase; laundry; detergent; textile desizing;
XX KW sweetener production; ethanol production; brewing; paper production.
XX
XX OS Bacillus sp.
XX
XX PN W0200060060-A2.
XX
XX PD 12-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-DK000149.
XX
XX 31-MAR-1999; 99DK-00000439.
PR 13-APR-1999; 99DK-00000490.
PR 13-APR-1999; 99US-00290734.
XX
XX (NOVO ) NOVO NORDISK AS.
XX
XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
XX Bisgaard-Frantzen H, Svendsen A, Andersen C;
XX
XX WPI; 2001-006814/01.
DR N-PSDB; AAC63114.
XX
XX New polypeptides having alpha-amylase activity and nucleic acids encoding
XX the enzymes, useful as a detergent or a dishwash detergent composition,
XX for textile desizing, for liquefaction of starch, or for ethanol
XX production.
XX
XX Claim.3; Page 106-108; 116pp; English.
XX
XX The present invention relates to proteins having alpha-amylase activity
XX and their coding sequences. These proteins are useful in a number of
XX industrial applications, including detergents, hard surface cleaning
XX compositions, in compositions for desizing textiles, fabrics and
XX garments, in the production of pulp and paper, in beer-making and
XX brewing, and in starch conversion processes such as sweetener and ethanol

```

CC	production	PI	Bisgard-Frantzen H, Svendsen A, Andersen C;
XX		XX	
SQ	Sequence 485 AA;	DR	WPI: 2001-006814/01.
		DR	N-PSDB; AAC63115.
		XX	New polypeptides having alpha-amylase activity and nucleic acids encoding
		PT	the enzymes, useful as a detergent or a dishwash detergent composition,
		PT	for textile desizing, for liquefaction of starch, or for ethanol
		PT	production.
		XX	
		XX	Claim 3; Page 111-112; 116pp; English.
		XX	The present invention relates to proteins having alpha-amylase activity
		CC	and their coding sequences. These proteins are useful in a number of
		CC	industrial applications, including detergents, hard surface cleaning
		CC	compositions, in compositions for desizing textiles, fabrics and
		CC	garments, in the production of pulp and paper, in beer-making and
		CC	brewing, and in starch conversion processes such as sweetener and ethanol
		CC	production
		XX	
		SQ	Sequence 485 AA;
			Query Match 96.7%; Score 2613; DB 4; Length 485;
			Best Local Similarity 95.5%; Pred. No. 2e-211;
			Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA 60		
DB	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA 60		
QY	61 YLDYDLGEFNQKGTVRTKYGTRSQLQAAVTSLNKNGIQVYGVVMNHKGGADATEMVRV 120		
DB	61 YLDYDLGEFNQKGTIRTKYGTENQLQAAVNALKSGIQVYGVVMNHKGGADATEMVRV 120		
QY	121 EVNPNRNQEVTSGEYTIETATRPDPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF 180		
DB	121 EVNPNRNQEVTSGEYTIETATRPDPGRGNTHSNFKRWYHFDGVWDQSRKLNNRIYKF 180		
QY	181 RHGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240		
DB	181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240		
QY	241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAIENYLKTNWNSHVSFVDFPLHYNLYNA 300		
DB	241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAIENYLKTNWNSHVSFVDFPLHYNLYNA 300		
QY	301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360		
DB	301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360		
QY	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILAEARQKAYAGKONDYLDHNNIIGWTREGNTA 420		
DB	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILAEARQKAYAGKONDYLDHNNIIGWTREGNTA 420		
QY	421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480		
DB	421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480		
QY	481 IWVWK 485		
DB	481 IWVWK 485		
		RESULT 12	
		ABB06938	
		ID	ABB06938 standard; protein; 485 AA.
		XX	
		AC	ABB06938;
		XX	
		DT	19-JUN-2002 (first entry)
		XX	
		DE	Bacillus termamyl-like alpha-amylase protein SEQ ID NO:12.
		XX	
CC	production	PI	Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
XX		XX	
SQ	Sequence 485 AA;	DR	WPI: 2001-006814/01.
		DR	N-PSDB; AAC63115.
		XX	New polypeptides having alpha-amylase activity and nucleic acids encoding
		PT	the enzymes, useful as a detergent or a dishwash detergent composition,
		PT	for textile desizing, for liquefaction of starch, or for ethanol
		PT	production.
		XX	
		XX	Claim 3; Page 111-112; 116pp; English.
		XX	The present invention relates to proteins having alpha-amylase activity
		CC	and their coding sequences. These proteins are useful in a number of
		CC	industrial applications, including detergents, hard surface cleaning
		CC	compositions, in compositions for desizing textiles, fabrics and
		CC	garments, in the production of pulp and paper, in beer-making and
		CC	brewing, and in starch conversion processes such as sweetener and ethanol
		CC	production
		XX	
		SQ	Sequence 485 AA;
			Query Match 96.7%; Score 2613; DB 4; Length 485;
			Best Local Similarity 95.5%; Pred. No. 2e-211;
			Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGITAVWIPPAWKASQNDVGYGA 60		
DB	1 HHNGTGTMMQYFEWYLPNDGNHNRNLSDASNLKSGISAVWIPPAWKASQNDVGYGA 60		
QY	61 YLDYDLGEFNQKGTVRTKYGTRSQLQAAVTSLNKNGIQVYGVVMNHKGGADATEMVRV 120		
DB	61 YLDYDLGEFNQKGTIRTKYGTENQLQAAVNALKSGIQVYGVVMNHKGGADATEMVRV 120		
QY	121 EVNPNRNQEVTSGEYTIETATRPDPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKF 180		
DB	121 EVNPNRNQEVTSGEYTIETATRPDPGRGNTHSNFKRWYHFDGVWDQSRKLNNRIYKF 180		
QY	181 RHGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240		
DB	181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240		
QY	241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAIENYLKTNWNSHVSFVDFPLHYNLYNA 300		
DB	241 IKYSFTRDWINHVRSAATGKNMFAVEFKNDLGAIENYLKTNWNSHVSFVDFPLHYNLYNA 300		
QY	301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360		
DB	301 SKSGGNYDMRNIFNGTVVQRHPHSAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360		
QY	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILAEARQKAYAGKONDYLDHNNIIGWTREGNTA 420		
DB	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILAEARQKAYAGKONDYLDHNNIIGWTREGNTA 420		
QY	421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480		
DB	421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480		
QY	481 IWVWK 485		
DB	481 IWVWK 485		
		RESULT 11	
		AAB29261	
		ID	AAB29261 standard; protein; 485 AA.
		XX	
		AC	AAB29261;
		XX	
		DT	07-FEB-2001 (first entry)
		XX	
		DE	Bacillus sp. alpha-amylase #2.
		XX	
		KW	Alpha-amylase; laundry; detergent; textile desizing;
		KW	sweetener production; ethanol production; brewing; paper production.
		XX	
		OS	Bacillus sp.
		XX	
		PN	WO200060060-A2.
		XX	
		PD	12-OCT-2000.
		XX	
		PP	28-MAR-2000; 2000WO-DX000149.
		XX	
		PR	31-MAR-1999; 99DK-00000439.
		PR	13-APR-1999; 99DK-00000490.
		PR	13-APR-1999; 99US-00290734.
		XX	
		PA	(NOVO) NOVO NORDISK AS.
		XX	

Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1; variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent; washing; sweetener; ethanol; starch.

Bacillus sp.

W0200166712-A2.

13-SEP-2001.

07-MAR-2001; 2001WO-DK000144.

08-MAR-2000; 2000DK-00000376.

15-MAR-2000; 2000US-0189857P.

23-FEB-2001; 2001DK-00000303.

26-FEB-2001; 2001US-0271382P.

(NOVO) NOVOZYMES AS.

Andersen C, Borchert TV, Nielsen BR;

WPI; 2002-239612/29.

N-PSDB; ABL50569.

Novel variant of parent termamyl-like alpha-amylase useful as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.

Claim 1; Page 148-149; 153pp; English.

The present invention describes a variant of a parent termamyl-like alpha amylase (EC 3.2.1.1) (I) comprising an alteration at one or more positions of a group of 31 possible amino acid positions. The alteration in (I) may be at Arg28, Arg118, Asn174, Asn181, Gly182, Asp183, Gly184, Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306, Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444, Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for washing and/or dishwashing, textile desizing, and starch liquefaction. (I) is useful as a component in hard surface cleaning detergent composition, and for producing sweeteners and ethanol from starch. (I) has altered solubility, preferably increased solubility, in particular under washing, dish washing or hard surface cleaning conditions. The present sequence represents a Bacillus termamyl-like alpha-amylase which is used in the exemplification of the present invention

Sequence 485 AA;

Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRNLSASNLKSGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLVLDGEFNQKVTYKTRSLQLOAAVTSLNKNGIQVYGVVNVNHHKGGADATFEMVRV 120
DB 61 YDLVLDGEFNQKVTYKTRSLQLOAAVNAKNGIQVYGVVNVNHHKGGADATFEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTTAEATWTFPPGGRGNTHSFKWRVYHFDGVDWQSRRLANNRYKF 180
DB 121 EVNPNRNRQEVGTGEYTTAEATWTFPPGGRGNTHSFKWRVYHFDGVDWQSRRLANNRYKF 180
QY 181 RGHGKAWDEVDTEGNYDYLMYADIDMDHPEVVNLRNNGWYVNTLTGLDGFPRIDAVKH 240
DB 181 RGDCKGWDEVDTEGNYDYLMYADIDMDHPEVVNLRNNGWYVNTLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWLNHVRSAATGKNFAVAFWQNDLGAENLYQTNHNSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWLNHVRSAATGKNFAVAFWQNDLGAENLYQTNHNSVDFVPLHYNLYNA 300
QY 301 SKSGNGYDMRINFNGTVVQRHPHSHAVTFVDNHDSPPEALESFVEWFKPLAYALTLTRE 360

Db 301 SKSGNGYDMRINFNGTVVQRHPHSHAVTFVDNHDSPPEALESFVEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGYGIPTHGVPMARSKIDPILFAROKYAYGKONDYLDHNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGYGIPTHGVPMARSKIDPILFAROKYAYGKONDYLDHNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFMVGRNKGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWNVK 485
DB 481 IWNVK 485

RESULT 13
AAU12154
ID AAU12154 standard; protein; 485 AA.
XX AC AAU12154;
XX DT 09-APR-2002 (first entry)
XX DE Bacillus TERMAMYL-like alpha-amylase AA560.
XX KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
XX KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
XX KW amylopectin; limit dextrin; NOVAMYL; AA560.
XX OS Bacillus sp.
XX PN W0200188107-A2.
XX PD 22-NOV-2001.
XX PF 10-MAY-2001; 2001WO-DK000323.
XX PR 12-MAY-2000; 2000DK-00000779.
XX PA (NOVO) NOVOZYMES AS.
XX PI Svendsen A, Jorgensen CT, Nielsen BR;
XX DR WPI; 2002-106123/14.
XX DR N-PSDB; AAS20027.
XX PT New variant of parent Termamyl-like alpha-amylase for use as a component in washing and dishwashing compositions, for textile desizing, for starch liquefaction, and for producing sweeteners and ethanol from starch.
XX PS Claim 5; Page 78-81; 84pp; English.
XX CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339, or at position 234, where the variant has alpha-amylase activity and each position corresponds to a position of a parent Termamyl-like alpha- amylase sequence having a Bacillus licheniformis alpha-amylase sequence of 483 amino acids, given in specification. The variant alpha- amylase, a detergent additive comprising the variant or a detergent composition comprising the variant, is useful for washing and/or dishwashing or textile desizing. The alpha- amylase is useful for starch liquefaction or ethanol production and as a component in a hard surface cleaning detergent composition, and for producing sweeteners from starch. The variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic branch linkage cleavage activity of amylopectin or a limit dextrin prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a natural variant of the TERMAMYL alpha- amylase, AA560

Sequence 485 AA;

Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;

XX Termamyl; alpha amylase; starch liquefaction; ethanol production;
KW textile desizing; detergent; enzyme.
XX
OS Bacillus sp.
XX
PN WO200210355-A2.
XX
PD 07-FEB-2002.
XX
XX 12-JUL-2001; 2001WO-DK000488.
XX
XX 01-AUG-2000; 2000DK-00001160.
PR 12-SEP-2000; 2000DK-00001354.
PR 10-NOV-2000; 2000DK-00001687.
PR 26-APR-2001; 2001DK-00000655.
XX
XX (NOVO) NOVOZYMES AS.
XX
XX Thisted T, Kjaerulff S, Andersen C, Fugleang CC;
XX
XX WPI; 2002-280633/32.
DR N-PSDB; ABL96212.
XX
XX Variant of parent Termamyl-like alpha amylase, useful in detergent
PT compositions, for starch liquefaction, ethanol production, washing and/or
PT dish washing, and textile desizing.
XX
XX Claim 8; Page 75-76; 90pp; English.
XX
XX This invention relates to variants of a parent Termamyl-like alpha-
CC amylases. These are used for starch liquefaction, ethanol production,
CC detergent, and textile desizing. The amylases have altered stability,
CC particularly at high temperatures from 70-120plusOC and low pH in the
CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
CC amylase
XX
XX Sequence 485 AA;

Query Match 96.7%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 2e-211;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLRSASNLKSGISAVWIPPAWKASQNDVGGA 60
QY 61 YDLYDLGFEFNQKGTVRTKYGTRSQLOAAVTSKXNGIQVYGDVVVNHKGGADATMVRV 120
DB 61 YDLYDLGFEFNQKGTVRTKYGTRNQLOAAVNAKLSNGIQVYGDVVVNHKGGADATMVRV 120
QY 121 EVNPNRNRQEVTEYTTAEATRPDPGKGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTTAEATKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGHGKAWDWEVDTENGNYDLYMYADI DMHDPVVNLELNMGVWYTTNLGLDGFRI DAVKH 240
DB 181 RGDGKGWDWEVDTENGNYDLYMYADI DMHDPVVNLELNMGVWYTTNLGLDGFRI DAVKH 240
QY 241 IKYSFTFDWINHVRSAFGKMFVAEFAEKNDLGAENYLOKTNWNSHFDVPLHNLNYNA 300
DB 241 IKYSFTFDWINHVRSAFGKMFVAEFAEKNDLGAENYLNKTNWNSHFDVPLHNLNYNA 300
QY 301 SKSGGNDYDMENIENGTVVQRHPSHVTVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
DB 301 SKSGGNDYDMQIENGTVVQRHPSHVTVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGYDYGIPTHGVPMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480

Db 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVVK 485
Db 481 IWVVK 485
Search completed: October 7, 2004, 00:12:25
Job time : 59.5516 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-13
Perfect score: 2703
Sequence: 1 HHNGTGTMMQYFEWLPND.....ADGNGFVNGSGSVIWNK 485
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2703	100.0	518	1 A27705	alpha-amylase (EC
2	1876	69.4	512	1 ALBSL	alpha-amylase (EC
3	1874.5	69.3	549	1 A54541	alpha-amylase (EC
4	1867.5	69.1	549	1 A24549	alpha-amylase (EC
5	1866.5	69.1	549	1 A24436	alpha-amylase (EC
6	1836	67.9	514	1 ALBSN	alpha-amylase (EC
7	1817	67.2	548	1 ALBSF	alpha-amylase (EC
8	1360	50.3	493	2 S15713	alpha-amylase (EC
9	1280	47.4	484	2 G95160	alpha-amylase (imp
10	1278	47.3	484	2 P98026	alpha-amylase (EC
11	1275	47.2	492	2 AH2079	alpha-amylase (imp
12	1139	42.1	491	2 C86781	alpha-amylase (imp
13	1125	41.6	506	2 G98247	cytoplasmic alpha-
14	1124	41.6	495	2 AD3038	alpha-amylase (imp
15	1074	39.7	494	1 B45738	alpha-amylase (EC
16	1064	39.4	494	2 AD0751	cytoplasmic alpha-
17	1054	39.0	495	2 B90982	cytoplasmic alpha-
18	1045	38.7	495	1 A45738	alpha-amylase (EC
19	1035	38.3	495	2 B85810	cytoplasmic alpha-
20	362.5	13.4	217	2 A19506	alpha-amylase (EC
21	331	12.2	1196	2 A29130	beta-amylase (EC 3
22	311.5	11.5	482	2 S31478	alpha-amylase (EC
23	285	10.5	504	2 A55861	alpha-amylase (EC
24	281.5	10.4	421	2 S10514	alpha-amylase (EC
25	277	10.2	423	2 T09942	alpha-amylase (EC
26	276	10.2	440	2 S14958	alpha-amylase (EC
27	266.5	9.9	435	2 J07137	alpha-amylase (EC
28	266	9.8	826	2 E96720	probable alpha-amy
29	265	9.8	437	2 S14956	alpha-amylase (EC

30	265	9.8	438	2	S14957	alpha-amylase (EC
31	264.5	9.8	435	2	S12625	glucan 1,4-alpha-m
32	263.5	9.7	551	2	S05667	alpha-amylase (EC
33	261	9.7	428	2	T05521	alpha-amylase (EC
34	258	9.5	427	1	ALBHB	alpha-amylase (EC
35	258	9.5	429	1	JE0406	alpha-amylase (EC
36	256.5	9.5	499	1	ALAS3	alpha-amylase (EC
37	256.5	9.5	499	2	JN0588	alpha-amylase (EC
38	255	9.4	413	1	ALMT3	alpha-amylase (EC
39	254	9.4	439	2	T02956	alpha-amylase (EC
40	253.5	9.4	498	2	A48305	alpha-amylase (EC
41	253.5	9.4	499	2	B48305	alpha-amylase (EC
42	253.5	9.4	499	2	JT0466	alpha-amylase (EC
43	253	9.4	478	2	JK0201	alpha-amylase (EC
44	252.5	9.3	428	2	S10013	alpha-amylase (EC
45	252.5	9.3	434	2	S12775	alpha-amylase (EC

ALIGNMENTS

RESULT 1

A27705
alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A;Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic
A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705
A;Molecule type: DNA
A;Residues: 1-518 <TSU>
A;Cross-references: GB:M18862; NID:gi42496; PID:AAA22231.1; PID:gi42497
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2703; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.9e-179;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	HHNGTGTMMQYFEWLPNDGNHNRLNSDASLKSIGITAVWIPPAWKASQNDVGYGA	60
Db	34	HHNGTGTMMQYFEWLPNDGNHNRLNSDASLKSIGITAVWIPPAWKASQNDVGYGA	93
Qy	61	YDLYDLGEFQKGTVRTKYGTRSQLOAAVTSLKNGIGQVYGDVVMNHKGGADATEMVR	120
Db	94	YDLYDLGEFQKGTVRTKYGTRSQLOAAVTSLKNGIGQVYGDVVMNHKGGADATEMVR	153
Qy	121	EVNPNNRNQVTEGYTTEAWTRFDPGRGNTHSFKWRVHFPGVDVMDQSRRLNNRIYKF	180
Db	154	EVNPNNRNQVTEGYTTEAWTRFDPGRGNTHSFKWRVHFPGVDVMDQSRRLNNRIYKF	213
Qy	181	RGHGKAWDEVDTEGNYDLYMADIDMDPEVNNELRNWGVWYNTLTGLDGRIDAVKH	240
Db	214	RGHGKAWDEVDTEGNYDLYMADIDMDPEVNNELRNWGVWYNTLTGLDGRIDAVKH	273
Qy	241	IKYSFTRDWLNHVRSAATKKNFAVAEFPKNDLGAENYLOKTNWHSVDFVPLHLYNA	300
Db	274	IKYSFTRDWLNHVRSAATKKNFAVAEFPKNDLGAENYLOKTNWHSVDFVPLHLYNA	333

QY 301 SKSGNVDNRNI FNGTVVQHPHSHAVTFVDNHDSDPBEALESFVEEFPKPLAYALTITRE 360
|||||
Db 334 SKSGNVDNRNIFNGTVVQHPHSHAVTFVDNHDSDPBEALESFVEEFPKPLAYALTITRE 393
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QY 361 QGYPSVFYGDYIGPTGHPVPMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
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Db 394 QGYPSVFYGDYIGPTGHPVPMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 453
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QY 421 HPNSGLATINS DGAGGSKMFWGVRNKGAGQVMSDITGNRTGTGTINADGWGNFVNGGSVS 480
|||||
Db 454 HPNSGLATINS DGAGGSKMFWGVRNKGAGQVMSDITGNRTGTGTINADGWGNFVNGGSVS 513
|||||
QY 481 IWNK 485
|||||
Db 514 IWNK 518
|||||

RESULT 2

ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus licheniformis
C;Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
C;Accession: A91997; B24549; A21663; I39774; I39772; A26151; S53788; A00844
R;Yuuki, T.; Nomura, T.; Tezuka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Ueda, S.
J. Biochem. 98, 1147-1156, 1985
A;Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylases deduced from the DNA sequences.
A;Reference number: A91997; MUID:86111694; PMID:2418011
A;Accession: A91997
A;Molecule type: DNA
A;Residues: 1-162, 'R', 164-512 <YUU>
A;Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
A;Experimental source: NCIB 27811
R;Gray, G.L.; Mainzer, S.E.; Ray, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: B24549
A;Molecule type: DNA
A;Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
A;Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
A;Experimental source: NCIB 8061
R;Stephens, M.A.; Ortlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J. Bacteriol. 158, 369-372, 1984
A;Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase gene
A;Reference number: A91796; MUID:84185455; PMID:6609154
A;Accession: A91796
A;Molecule type: DNA
A;Residues: 1-104 <STE>
A;Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R;Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
A;Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase gene
A;Reference number: A21663; MUID:85076654; PMID:6334606
A;Accession: A21663
A;Molecule type: DNA
A;Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 81-104, 'L', 106-110, 'S', 112-113, 'S', 115-116, 'S', 118-119, 'S', 121-122, 'S', 124-125, 'S', 127-128, 'S', 130-131, 'S', 133-134, 'S', 136-137, 'S', 139-140, 'S', 142-143, 'S', 145-146, 'S', 148-149, 'S', 151-152, 'S', 154-155, 'S', 157-158, 'S', 160-161, 'S', 163-164, 'S', 166-167, 'S', 169-170, 'S', 172-173, 'S', 175-176, 'S', 178-179, 'S', 181-182, 'S', 184-185, 'S', 187-188, 'S', 190-191, 'S', 193-194, 'S', 196-197, 'S', 199-200, 'S', 202-203, 'S', 205-206, 'S', 208-209, 'S', 211-212, 'S', 214-215, 'S', 217-218, 'S', 220-221, 'S', 223-224, 'S', 226-227, 'S', 229-230, 'S', 232-233, 'S', 235-236, 'S', 238-239, 'S', 241-242, 'S', 244-245, 'S', 247-248, 'S', 250-251, 'S', 253-254, 'S', 256-257, 'S', 259-260, 'S', 262-263, 'S', 265-266, 'S', 268-269, 'S', 271-272, 'S', 274-275, 'S', 277-278, 'S', 280-281, 'S', 283-284, 'S', 286-287, 'S', 289-290, 'S', 292-293, 'S', 295-296, 'S', 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Db 390 VFYGDYMG--TKGDSQREIPALKKHKEIPILKARKQYAYGAQHDFDHHDIVGWTRGDS 447
QY 421 HPNSGLATIMSDGAGGSKWVFGRNKAGQVMSDITGRTGTVTINADGWNFSVNGGSVS 480
Db 448 VANSGLAALITDGGGAKMYVGRQNAGETWHDITGNRSEPVVINSRGWGEFHVNGGSVS 507
QY 481 IWNK 485
Db 508 IYVQ 512

RESULT 3
A54541
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNL1792)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C/Accession: A54541
R/Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A/Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A/Reference number: A54541
A/Accession: A54541
A/Molecule type: DNA
A/Residues: 1-549 <JOR>
A/Cross-references: GB:X59476
A/Experimental source: chromosomal DNA of strain DNL1792
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status predicted <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.3%; Score 1874.5; DB 1; Length 549;
Best Local Similarity 67.2%; Pred. No. 1.3e-121;
Matches 321; Conservative 76; Mismatches 80; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITATWIPPANKGASQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGVYDLYD 98
QY 66 LGFBNQKGTVRTKGTGTRSQLQAQAVTSLKNNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFBNQKGTVRTKGTGTRSQLQAQAVTSLKNNGIQYGVDMVNMHKGADATEMVRVAVENPN 158
QY 126 NRNQVETGEYTIETAWTRFDPFGNGTHSSFKRWYHFDGVDWDSRLNRIYKFRGHGK 185
Db 159 DRNQISGTYQIQAWTKFDPFGNGTYSFQKRWYHFDGVDWDSRLNRIYKFRGIGK 217
QY 186 AWDWEVDTEGNDYLMYADIDMDHPVNMELRWGVMYNTLGLDGFRLDAVKHIKYSF 245
Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNMELRWGVMYNTLGLDGFRLDAVKHIKFSF 277
QY 246 TRDWINHVRSGTKNMFAEAFWKNDI:GATENYLQKTNWNSHVPDVLPHYLNYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEIWSYDINKLHNYITKDTGWSLFDAPLHKNFYTASKSGG 337
QY 306 NYDMRNINFGTVQRHPSHVAFTVDNDSOPEEALESFVBWEKFLAYALTLTREQGYPS 365
Db 338 AFDMRLTWTLMKQDTLAVTFVDNHDTEPGALQSWDPWFKFLAYALTREQGYPC 397
QY 366 VFYGDYGYIPTHGVPMRSKIDPILFARQYKQKNDYLDHNNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGYIPTHGVPMRSKIDPILFARQYKQKNDYLDHNNIIGWTRGNTAHNPSG 457

QY 426 LATIMSDGAGGSKWVFGRNKAGQVMSDITGRTGTVTINADGWNFSVNGGSVSIVW 483
Db 458 LAALITDGGGSKWYVGRQNAGETWHDITGNRSDTGTVTINSDGWNFSVNGGSVSIVW 515

RESULT 4
A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: A24549; I39501; I39770
R/Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A/Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother
A/Reference number: A91817; MUID:86195857; PMID:3009417
A/Accession: A24549
A/Molecule type: DNA
A/Residues: 1-549 <GRA>
A/Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513
A/Experimental source: genomic DNA of strain NZ-3
R/Sato, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A/Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distar
A/Reference number: I39501; MUID:88139156; PMID:3257753
A/Accession: I39501
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 536-549 <RES>
A/Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A/Experimental source: strain DY-5
A/Accession: I39770
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 536-549 <RE2>
A/Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A/Experimental source: strain 799
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status predicted <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.1%; Score 1867.5; DB 1; Length 549;
Best Local Similarity 67.2%; Pred. No. 3.9e-121;
Matches 321; Conservative 75; Mismatches 81; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITATWIPPANKGASQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLTKVANEANLSSLGITALLWLPAYKGTSDVGYGVYDLYD 98
QY 66 LGFBNQKGTVRTKGTGTRSQLQAQAVTSLKNNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFBNQKGTVRTKGTGTRSQLQAQAVTSLKNNGIQYGVDMVNMHKGADATEMVRVAVENPN 158
QY 126 NRNQVETGEYTIETAWTRFDPFGNGTHSSFKRWYHFDGVDWDSRLNRIYKFRGHGK 185
Db 159 DRNQISGTYQIQAWTKFDPFGNGTYSFQKRWYHFDGVDWDSRLNRIYKFRGIGK 217
QY 186 AWDWEVDTEGNDYLMYADIDMDHPVNMELRWGVMYNTLGLDGFRLDAVKHIKYSF 245
Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNMELRWGVMYNTLGLDGFRLDAVKHIKFSF 277
QY 246 TRDWINHVRSGTKNMFAEAFWKNDI:GATENYLQKTNWNSHVPDVLPHYLNYNASKSGG 305

Db 278 FPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMENFNGTVQVRHPSHVAFTVDNHDSPQEALESFVEWPKFLAYALTTLTREQQYPS 365
Db 338 AFDMSTLNNLTKMDQTLAVTFVDNHDTEFGQALQSWDPWPKFLAYAFILTRQEGYPC 397
QY 366 VFYGDYGYGIPTHGVPMRMSKIDPILFARQYAYGKQNDYLDHNNIIGWTREGNTAHPNSG 425
Db 398 VFYGDYGYGIPQYNIPLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGAGSKMVFGRNKAQOWSDITGNRTGTVTINADGNGFNSVNGSVSIWV 483
Db 458 LAALITDGGSGKMWYVGQHAGKVFYDLTGNRSDTVTINSDGNGEFGKNGSVSVWV 515
RESULT 5
A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24436; I39777
R;Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A;Reference number: A24436; MUID:85234394; PMID:3924897
A;Molecule type: DNA
A;Accession: A24436
A;Residues: 1-549 <NAK>
A;Cross-references: GB:M11450
A;Experimental source: plasmid pAT5
A;Note: amino end of the mature protein also determined
R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.
Gene 96, 37-41, 1990
A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid con
A;Reference number: I39772; MUID:91092499; PMID:2265757
A;Accession: I39777
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Gene: amyS
A;Genome: plasmid
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
F;1-34/Domain: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysacc
F;35-549/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted
Query Match 69.1%; Score 1866.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 4.5e-121;
Matches 320; Conservative 75; Mismatches 82; Indels 1; Gaps 1;
QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGAYDLYD 65
Db 39 NGTMMQYFEWYLPDDGLTGLTKVANEANLSSGLITALLPFPAYKGTSRSDVGIVTDLYD 98
QY 66 LGFBNQKGTVRTKYGRSLQAAVTSLNKNGIQYGVGVVNNHKGADATEMTRAVEVNPV 125
Db 99 LGFBNQKGTVRTKYGRSLQAAVTSLNKNGIQYGVGVVNNHKGADATEMTRAVEVNPV 158
QY 126 NRQEVTEGVTIBAWTRFDPFGNGNTHSSPKRWYHFDGVDVDDQSRNLNRRNRYKFRGHGK 185
Db 159 DRNQETISGTTQIQAWTKFDFPGRGNTYSSFKRWYHFDGVDVDDQSRNLNRRNRYKFRGIGK 217
QY 186 AMDWEVDTENGNYDLYMAYDIDMDHPVNVNLRNNGVWYNTLTGLDGFRIIDAVKHKYSF 245

Db 218 AMDWEVDTENGNYDLYMAYDIDMDHPVNVNLRNNGVWYNTLTGLDGFRIIDAVKHKYSF 277
QY 246 TRDWINHVSATGKNFVAEFAWKNLDGALENVLOKTNHNSVFDYPLHYNLNASKSGG 305
Db 278 FPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYYITKTNGTMSLFDAPLHNKFTASKSGG 337
QY 306 NYDMENFNGTVQVRHPSHVAFTVDNHDSPQEALESFVEWPKFLAYALTTLTREQQYPS 365
Db 338 AFDMSTLNNLTKMDQTLAVTFVDNHDTEFGQALQSWDPWPKFLAYAFILTRQEGYPC 397
QY 366 VFYGDYGYGIPTHGVPMRMSKIDPILFARQYAYGKQNDYLDHNNIIGWTREGNTAHPNSG 425
Db 398 VFYGDYGYGIPQYNIPLSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSG 457
QY 426 LATIMSDGAGSKMVFGRNKAQOWSDITGNRTGTVTINADGNGFNSVNGSVSIWV 483
Db 458 LAALITDGGSGKMWYVGQHAGKVFYDLTGNRSDTVTINSDGNGEFGKNGSVSVWV 515
RESULT 6
ALBSN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus amylioliquefaciens
C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999
C;Accession: A92389; I39763; I39763; A00843
R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.
J. Biol. Chem. 258, 1007-1013, 1983
A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced fr
A;Reference number: A92389; MUID:83108808; PMID:6185474
A;Contents: PUB110
A;Accession: A92389
A;Molecule type: DNA
A;Residues: 1-514 <TAK>
A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:g142428; PIDN:AAA221;
R;Chung, H.S.; Friedberg, P.
Biochem. J. 185, 387-395, 1980
A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.
A;Reference number: A90307; MUID:80241725; PMID:6156671
A;Accession: A90307
A;Molecule type: protein
A;Residues: 32-53,'I',55-63,'L',65-78,'D',80-83,'S',85-222 <CHU>
R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;
Gene 15, 43-51, 1981
A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t
A;Reference number: I39756; MUID:82051296; PMID:6170539
A;Accession: I39756
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298
R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.
Gene 59, 161-170, 1987
A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its ow
A;Reference number: I39763; MUID:88137952; PMID:2830166
A;Accession: I39763
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-39 <REG>
A;Cross-references: GB:M18424; NID:g142430; PIDN:AAA22192.1; PID:g142431
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-514/Product: alpha-amylase #status predicted <MPT>
F;229-362/Domain: alpha-amylase core homology <AMY>
F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted
F;262,292,359/Active site: Asp, Glu, Asp #status predicted
Query Match 67.9%; Score 1836; DB 1; Length 514;

Db 302 GANYDLRGFTDLSIVELKPKDKAVTFVDNHDRTQOGALSTVEWFKPAPYALILLRQDGL 361
Qy 364 PSFYGYGYGIP-THGVPAWMSKIDPILFARQKAYGQNDYLDHNNIIGTWREGTAHP 422
Db 362 PCVFGYGYGISOQAQDFKILDLRLAIRKDLAYGEQNDYDFHANCIGWVRSG--AEN 419
Qy 423 NSGLATMSDAGGSKWVFGRNKGAGQWSDITGNRTGTVTINADGWNFVSGGVSIIW 482
Db 420 QSPFVILISDQENSKMFVQGEWTNQTDFVLLGSHQGVTTIDEEGYQGFVPSARSVW 479

RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA073889.1; PID:gl7131281; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr2190
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 47.2%; Score 1275; DB 2; Length 492;
Best Local Similarity 50.2%; Pred. No. 2.4e-80;
Matches 246; Conservative 72; Mismatches 156; Indels 16; Gaps 5;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKG-ASQNDVGYGADLY 64
Db 5 NGTMMQYFEWYLPNDGNLMSKVESAPELADAGFTAWLPPAYKGPAGSDVGVGYDLP 64

Qy 65 DLGEFNQKGVTRTKYGRSLOQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRAVEVNP 124
Db 65 DLGEFDQKSGVTRTKYGRQVLDVAKSLQTHGLQVYADAVLNHMKGGDAVETPKATFPQ 124

Qy 125 NNRNQEVGYEITAEWTRFDPPGRCNTHSSFKRWYHFDGVDWDQSRRLNRIYKFRGHG 184
Db 125 DDRLNPKGGLQDKTYTHYFPGRQGYKSNFEMHWHFDDAVDYNEYS-GRDSTVYLLEG 183

Qy 185 KAWDWEYDTENGNDYLDYADIDMDHPEVNVNLRNKGWVYNTLGLDGRIDAVKHLYS 244
Db 184 KNFDYVALEKGNFAYLMGCDLDPQNEWVRGEVYWGKWLDTTKVDGFRIDAIKHISTW 243

Qy 245 FTRDWINHVSATGKNMFAVAFWKNLGAIENTYLOKTNMNSHVFDPVPLHYNLNASKSG 304
Db 244 FPEWIDALERHACKDLFMVGEYWNIDNTLLWYDVRGKMSVFDVPLHYNFHAQSKG 303

Qy 305 GNYDMRNIFNGTVVQRHPSHAFTVDNHDQPEALESFVEEWPFKPLAYALTITREQGYP 364
Db 304 GNYDMRRLDGTMMQRPSTHATVTVENHDSQPLQALESVVEPWPFKPLAYAILLRQEGYP 363

Qy 365 SVFVGDDYVGIPTHG-----VPAMRSKIDPILFARQKAYGQNDYLDHNNIIGW 413
Db 364 CVFHADYIAGYEYDNGKGNRYNIFMPSHRWIIDKLKYARKHAYGPOYNLDHNTIGW 423

Qy 414 TREGNTAHPNSGLATIMSDGAGGSKWVFGRNKGAGQWSDITGNRTGTVTINADGWNFS 473
Db 424 TRLGDAHP-QQMAVIMSDSGEGIKWMEVG--KNTKFDLTETHEIKAVYTNWGWGEFR 480

Qy 474 VNGGSVSIIW 483
Db 481 CLGGSVSVWV 490

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C:Accession: C86781

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich,

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: C86781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-491 <STO>

A:Cross-references: GB:AE005176; PID:gl2724224; PIDN:AAK05349.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: amyl

C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

RESULT 13

G98247

cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002

C:Accession: G98247

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: G98247

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-506 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L1863
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 41.6%; Score 1125; DB 2; Length 506;
Best Local Similarity 45.6%; Pred. No. 5.4e-70;
Matches 227; Conservative 77; Mismatches 170; Indels 24; Gaps 7;

QY 3 NGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGGAY 61
DB 11 NMAGRTLLQFFHYYPDGKLMSEVAEKAESLAKMGITDVMPLPAYKGAAGGYSVGYDY 70
QY 62 DLYDLGEFNGKQVTRTKYGRSOLQAQAVTSLKNGIQVYGDVVMNHKGGADATAMVRAVE 121
DB 71 DLPDLGEFDQKGVATKYGDRAALEHAGKTLKNGIRVHDVNLHKGGADEKEKVRVR 130
QY 122 VNPNNRQEVVTGEYTIETAWTRFDPGRGNTHSSFKRWYHFDGVDW-----DQSRRLNN 175
DB 131 VNPDDRDIIDDEFPALAYTRFTPPGRNGRHSKFIWDLKCFSGVDHIEEPTEDGIFRLVN 190
QY 176 RIYKRGHGAWEVDENGNDYLMYADIDMDHPEVNNELRWGVYVNTLGLDGFRI 235
DB 191 EY----GDGE-WNEEVDQENGFDYLMGADVFRNRAVYELKYWGRWLSQVQVDGFR 245
QY 236 DAVKHIKYSTROWINHVRSATGKMFVAFKNDLGAENYLOKTNWNSHSDVDFPLHY 295
DB 246 DAAKHIPAWFRDVGWGHMRETVPDLFVVAEYHWPDLKALSYLELVKQMLFDVALHH 305
QY 296 NLNASKSGGNYDMRNIFNGTVQVORHPSHVAFTVDNHDSDQPEALSFVEEWKPLAYAL 355
DB 306 SFHDASKQGGDFMRSIFDGLSVSAVDPDHAHTLVNDHDTQPLQSLAPVPEWPKPLAYAI 365
QY 356 TLREQGYPSVFGDYTG--LPTHGVPAMRSKID-----PILEARQYAYGKNDYL 405
DB 366 LLREEGVPCVFPDLFTGTSYTDGNDGNEYKIDIPALECLPKLIEARSFPANGPQTDIF 425
QY 406 DHNIIIGWREGTAHNSGLATIMSDGAGSKWMFVGRNKGQVMSDITGNRTGTIN 465
DB 426 DDASCTAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHREHITLD 483
QY 466 ADGWNFSVNGGSVIWV 483
DB 484 ESGGTPTNGGSSVWV 501

RESULT 14
AD3038
alpha-amylase amyA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3038
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3038
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-495 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: amyA
A;Map position: linear chromosome
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

Query Match 41.6%; Score 1124; DB 2; Length 495;

Best Local Similarity 45.8%; Pred. No. 6.1e-70;
Matches 226; Conservative 77; Mismatches 166; Indels 24; Gaps 7;

QY 8 TMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGYGAYDLYDL 66
DB 5 TLLQFFHYYPDGKLMSEVAEKAESLAKMGITDVMPLPAYKGAAGGYSVGYDYDLYDL 64
QY 67 GFNQKGTVTRTKYGRSOLQAQAVTSLKNGIQVYGDVVMNHKGGADATAMVRAVEVNN 126
DB 65 GFQDQKGVATKYGDRAALEHAGKTLKNGIRVHDVNLHKGGADEKEKVRVRVNPDD 124
QY 127 RQEVVTGEYTIETAWTRFDPGRGNTHSSFKRWYHFDGVDW-----DQSRRLNNRIYKF 180
DB 125 RTDIDDEFPALAYTRFTPPGRNGRHSKFIWDLKCFSGVDHIEEPTEDGIFRLVNEY--- 181
QY 181 RGHGKAWDEVDENGNDYLMYADIDMDHPEVNNELRWGVYVNTLGLDGFRI DAVKH 240
DB 182 -GDGE-WNEEVDQENGFDYLMGADVFRNRAVYELKYWGRWLSQVQVDGFRDLDAKH 239
QY 241 IKYSFTRDWINHVRSATGKMFVAFKNDLGAENYLOKTNWNSHSDVDFPLHYNLNA 300
DB 240 IPAWFRDVGWGHMRETVPDLFVVAEYHWPDLKALSYLELVKQMLFDVALHHSFHA 299
QY 301 SKSGGNYDMRNIFNGTVQVORHPSHVAFTVDNHDSDQPEALSFVEEWKPLAYALTRE 360
DB 300 SKQGGDFMRSIFDGLSVSAVDPDHAHTLVNDHDTQPLQSLAPVPEWPKPLAYAILRE 359
QY 361 QGYPSVFGDYTG--LPTHGVPAMRSKID-----PILEARQYAYGKNDYLDHNI 410
DB 360 EGVPCVFPDLFTGTSYTDGNDGNEYKIDIPALECLPKLIEARSFPANGPQTDIFDASC 419
QY 411 IGWREGTAHNSGLATIMSDGAGSKWMFVGRNKGQVMSDITGNRTGTINADGWSG 470
DB 420 IAFIRHGTADAP--GCVVVMSNGEPGEKQADLGPERRAGSVWRDFLGHREHITLDSGKG 477
QY 471 NFSVNGGSVIWV 483
DB 478 TPTNGGSSVWV 490

RESULT 15
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Salmonella typhimurium
C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: B45738
R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A;Reference number: A45738; MUID:93015717; PMID:1400215
A;Accession: B45738
A;Molecule type: DNA
A;Residues: 1-494 <RAH>
A;Cross-references: GB:I01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C;Genetics:
A;Gene: amyA
A;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F;202-335/Domain: alpha-amylase core homology <AMY>
F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.7%; Score 1074; DB 1; Length 494;
Best Local Similarity 43.1%; Pred. No. 1.7e-66;
Matches 212; Conservative 78; Mismatches 184; Indels 18; Gaps 6;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVMIPPAAWGASON-DVGYGAYDLY 64
DB 3 NPTLLQYFHWYPDGKLMSELAERADGLNDIGINWVLPAPACKGASGGYSVGYDYDLY 62


```
QY 65 DLGEFNOKGVTRKYGTRSQLAAVTSIKNGIOVYGDVWNNHKGAGADATEMVRAVEVNP 124
Db 63 DLGEFDQKGTATKYGDKRQLLTAIDALKKNIAVLDDVVVNNHKGGADEKERIRVQRVNQ 122
QY 125 NNRNQEVGTGTYTAEWTRFDPGGRGNTHSSGFKWYHFDGVDWDQSRRLNNRIYKFRGH- 183
Db 123 DDTQIDDDNIIECEGWTRYTFPARAGQYSFIWDYHCFSGIDHIEHPD-EDGIFKIYNDY 181
QY 184 -GKAWDEVTENGNYDYLADIDMDHPEVNVNLRNMGVYNTNLTGLDGFRIIDAVRHK 242
Db 182 TGDGWNQVDDMGNFYLMGENIDFRNHAVTEBIKYWARVWMEQTHCDGFRIDAVRHKIP 241
QY 243 YSFTRDWNVRSATGKMFVAFKNDLGAENYLOKTNWNSHVFDPVPLHYNLYNASK 302
Db 242 AWFYKEWIEHVQAVAPKPLFIVAEYWSHEVDKLTQYIDQVDGKTMLEFADPLQMKFHEASR 301
QY 303 SGGNYDMRNIFNGTVVORHPSHVTFFVDNHDSDPEEALSFVREWFKPLAYALTLTREQ 362
Db 302 QGAEYDMRHIPTGLVEADPFHAVTLVANHDTQPLQALEAPVEPWFPLAYALTLLRENG 361
QY 363 YPSVFGDYGYGIPTH-----GVPAMRSKIDPILBAROKYAYGKQNDYLDHNNII 411
Db 362 VPSVFYFDLYGASVEDSGENGETCRVDMPIV-NQLDRLLILARQRFPAHQIQTLPFDHNCI 420
QY 412 GWTREGNTAHPNSGLATIMSDAGGSKWMFVGRNKAQVMSDITGNRTGTVTINADQWGN 471
Db 421 AFSRSGTEENP--GCVVVLSNGDDGKTLILLGDNYANKTWDRDFSGNRDEYVVTNDQGEAT 478
QY 472 FSVNGSGSVSIWV 483
Db 479 FFCNAGSVSVWV 490
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Search completed: October 7, 2004, 00:20:49
Job time : 15.886 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTNGTMMQYFEPWLPND.....ADGWNFSVNGSVSIWVWK 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2703	100.0	518	1 AMT6_BACS7	P19571 bacillus sp
2	1876	69.4	512	1 AMY_BACLI	P06278 bacillus li
3	1866.5	69.1	549	1 AMY_BACST	P06279 bacillus st
4	1836	67.9	514	1 AMY_BACAM	P00692 bacillus am
5	1072	39.7	494	1 AMY2_SALTY	P26613 salmonella
6	1045	38.7	495	1 AMY2_ECOLI	P26612 escherichia
7	331	12.2	1196	1 AMYB_PAEPO	P21543 paenibacill
8	281.5	10.4	421	1 AMYA_VIGMU	P17859 vigna mungo
9	276	10.2	440	1 AM3A_ORYSA	P27932 oryza sativ
10	265	9.8	437	1 AM3C_ORYSA	P27939 oryza sativ
11	265	9.8	438	1 AM3B_ORYSA	P27937 oryza sativ
12	264.5	9.8	435	1 AM3D_ORYSA	P27933 oryza sativ
13	263.5	9.7	551	1 AMT4_PSSSA	P22963 pseudomonas
14	260	9.6	368	1 AMY3_HORVU	P04747 hordeum vul
15	259	9.6	548	1 AMT4_PSSST	P13507 pseudomonas
16	258	9.5	427	1 AMY2_HORVU	P04063 hordeum vul
17	258	9.5	429	1 AMY6_HORVU	P04750 hordeum vul
18	255	9.4	413	1 AMY3_WHEAT	P08117 triticum ae
19	254	9.4	719	1 AMY1_BACST	P19531 bacillus st
20	253.5	9.4	498	1 AMYA_ASAPW	Q02905 aspergillus
21	253.5	9.4	499	1 AMYB_ASAPW	Q02906 aspergillus
22	252.5	9.3	428	1 AMY1_ORYSA	P17654 oryza sativ
23	252.5	9.3	499	1 AMYA_ASPOS	P10529 aspergillus
24	251.5	9.3	499	1 AMYA_ASPSH	P30292 aspergillus
25	250	9.2	437	1 AM3E_ORYSA	P27934 oryza sativ
26	248	9.2	713	1 CDGT_BACSP	P30921 bacillus sp
27	247.5	9.2	438	1 AMY1_HORVU	P00693 hordeum vul
28	247.5	9.2	718	1 CDGT_BACCI	P30920 bacillus ci
29	246.5	9.1	713	1 CDGT_PAEWA	P31835 paenibacill
30	245.5	9.1	710	1 CDGT_THETU	P26827 thermoanaer
31	244	9.0	712	1 CDGT_BACSS3	P09121 bacillus sp
32	240.5	8.9	718	1 CDGT_BACSS	P31747 bacillus sp
33	240	8.9	713	1 CDGT_BACS8	P17692 bacillus sp

34	238	8.8	528	1	AMY_BACCI	P08137 bacillus ci
35	235	8.7	713	1	CDGT_BACCI	P43379 bacillus ci
36	234	8.7	713	1	CDGT_BACSO	P05618 bacillus sp
37	229	8.5	494	1	AMY1_SACFI	P21567 saccharomyc
38	228.5	8.5	442	1	MGTA_THENE	O86956 thermotoga
39	226.5	8.4	718	1	CDGT_BACLI	P14014 bacillus li
40	221.5	8.2	443	1	AMC2_ORYSA	P27935 oryza sativ
41	221.5	8.2	445	1	AMC2_ORYSA	P27941 oryza sativ
42	221	8.2	703	1	CDGT_BACS2	P31746 bacillus sp
43	220	8.1	564	1	AMY4_SCHPO	O94789 schizosach
44	219.5	8.1	711	1	CDGT_BACST	P31797 bacillus st
45	213.5	7.9	441	1	MGTA_THENA	P80099 thermotoga

ALIGNMENTS

RESULT 1

AMT6_BACS7	1	AMY_BACCI	1
ID	AMT6_BACS7	STANDARD;	PRT; 518 AA.
AC	P19571;		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amyase)		
DE	(Maltohexaoside-producing amylase) (Exo-maltohexaohydrolase).		
OS	Bacillus sp. (strain 707)		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1416;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.		
RX	MEDLINE=88162814; PubMed=3258152;		
RA	Takamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;		
RT	"Nucleotide sequence of the maltohexaoside-producing amylase gene from an alkalophilic Bacillus sp. #707 and structural similarity to liquefying type alpha-amyloses.";		
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).		
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages in amylaceous polysaccharides so as to remove successive maltohexaoside residues from the non-reducing chain ends.		
CC	-1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By similarity).		
CC	-1- PATHWAY: Starch degradation.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.		
CC	-----		
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CC	-----		
DR	EMBL; M18862; AAA22231.1; --		
DR	PIR; A27705; A27705.		
DR	HSP; P06278; 1VUS.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006046; Glyco_hydro_13.		
DR	Pfam; PF00128; alpha-amyase; 1_13.		
DR	PRINTS; PR00110; ALPHAAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
DR	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.		
FT	SIGNAL	1	33
FT	CHAIN	34	518
FT	ACT_SITE	269	269
FT	ACT_SITE	273	273
FT	ACT_SITE	366	366
FT	METAL	139	139
FT	METAL	196	196
FT	METAL	219	219
FT	GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.		
FT	BY SIMILARITY.		
FT	BY SIMILARITY.		
FT	BY SIMILARITY.		
FT	CALCIUM 1 (BY SIMILARITY).		
FT	CALCIUM 2 AND SODIUM (BY SIMILARITY).		
FT	CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).		

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FT METAL 221 221 CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT METAL 232 232 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 238 238 CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT METAL 240 240 CALCIUM 2 (BY SIMILARITY).
FT METAL 242 242 CALCIUM 2 (BY SIMILARITY).
FT METAL 273 273 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
Query Match 100.0%; Score 2703; DB 1; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.4e-178;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60
Db 34 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 93
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 94 YDLYDLGEFNQKGTVRTKYGTRSQLQAQVTSLNKNGIQVYGDVVMNHKGGADATEMVRV 153
QY 121 EVNPNNRNQVVTGEYTIETATRFDFPGRGNTSHSFKRWYHFDGVDQSDRRLLNNRIYKF 180
Db 154 EVNPNNRNQVVTGEYTIETATRFDFPGRGNTSHSFKRWYHFDGVDQSDRRLLNNRIYKF 213
QY 181 RHGKAWDEVDTEGNYDYLMTADIMDHPVVELNRKGVWYVYTLGLDGFRIDAVKH 240
Db 214 RHGKAWDEVDTEGNYDYLMTADIMDHPVVELNRKGVWYVYTLGLDGFRIDAVKH 273
QY 241 IKYSPTFDWLNHVRSATGKNMFAVEPKNDLGAENYLOKTNWNSVFDVPLHLYNNA 300
Db 274 IKYSPTFDWLNHVRSATGKNMFAVEPKNDLGAENYLOKTNWNSVFDVPLHLYNNA 333
QY 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 360
Db 334 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEWFKPLAYALTLTRE 393
QY 361 QGYPSVFGYGYGIPTHGVPAWMSKIDPILAEARKQYAGKQNDYLDHNNIIGWTRGNTA 420
Db 394 QGYPSVFGYGYGIPTHGVPAWMSKIDPILAEARKQYAGKQNDYLDHNNIIGWTRGNTA 453
QY 421 HPNSGLATIMSDGAGGSKWPFVGRNKAGQVWSDITGNRTGTVTINADGWNFSGVSGVS 480
Db 454 HPNSGLATIMSDGAGGSKWPFVGRNKAGQVWSDITGNRTGTVTINADGWNFSGVSGVS 513
QY 481 IWVWK 485
Db 514 IWVWK 518
RESULT 2
AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; Q84171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=8611694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Ueda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences."
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RL J. Biochem. 98:1147-1156 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX Shahhosseini M., Ziaei A.A., Ghaemi N., Pourbabaei A.A.;
RA "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372 (1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442 (1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373 (1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltooligosaccharide substrates.";
RL FEBS Lett. 518:79-82 (2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488 (1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037 (1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057 (2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RESULT 3
AMY_BACST
ID AMY_BACST STANDARD; PRT; 549 AA.
AC P06279; Q45519;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
GN glucanohydrolase).
OS Amylase.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.
RX MEDLINE=85234394; PubMed=3924897;
RA Nakajima R., Imanaka T., Aiba S.;
RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
RT gene";
RL J. Bacteriol. 163:401-406(1985).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=DY5/PHI300;
RA Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:
RT homology between prokaryotic and eukaryotic alpha-amylases at the
RT active sites.";
RL J. Biochem. 98:95-103(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=N2-3;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requa C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;
RA "Thermotable alpha amylase of Bacillus stearothermophilus: cloning,
RA expression, and secretion by Escherichia coli.";
RL (In) Chaloupka J., Krumphanz V. (eds.);
RA Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,
RA New York (1987).
RN [5]
RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.
RX STRAIN=DY-5;
RA MEDLINE=86059211; PubMed=2999073;
RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,
RA Idota Y., Yamagata H., Uda S.;
RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by
RT protein-producing Bacillus brevis 47 carrying the Bacillus
RT stearothermophilus amylase gene";
RL J. Bacteriol. 164:1182-1187(1985).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=21125602; PubMed=11226887;
RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;
RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:
RT possible factors determining the thermostability.";
CC CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M11450; AAA22235.2; -
DR EMBL; X02769; AAA26547.1; -
DR EMBL; M57457; AAA22227.1; -
DR EMBL; M13255; AAA22241.1; -
DR PIR; A24436; A24436.
DR PIR; A91999; ALBSP.
DR PDB; 1HVX; 05-AUG-03.
DR InterPro; IPR006589; Alp amyl_cat sub.
DR InterPro; IPR006047; Alpha amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 34
FT CHAIN 35 549 ALPHA-AMYLASE.
FT ACT_SITE 268 268
FT ACT_SITE 272 272
FT ACT_SITE 365 365
FT METAL 139 139
FT METAL 196 196
FT METAL 218 218
FT METAL 220 220
FT METAL 231 231
FT METAL 237 237
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FT METAL 272 272
FT METAL 337 337
FT METAL 339 339
FT METAL 440 440
FT METAL 441 441
FT METAL 464 464
FT CONFLICT 13 13 M -> V (IN REF. 3).
FT CONFLICT 19 19 L -> W (IN REF. 3).
FT CONFLICT 23 23 L -> S (IN REF. 2 AND 3).
FT CONFLICT 31 31 P -> H (IN REF. 2 AND 5).
FT CONFLICT 107 107 A -> T (IN REF. 2 AND 3).
FT CONFLICT 167 167 T -> I (IN REF. 4).
FT CONFLICT 179 179 P -> N (IN REF. 3).
FT CONFLICT 251 251 S -> N (IN REF. 2, 3 AND 4).
FT CONFLICT 260 262 TNI -> RTL (IN REF. 4).
FT CONFLICT 284 284 D -> Y (IN REF. 2, 3 AND 4).
FT CONFLICT 312 312 M -> T (IN REF. 2 AND 3).
FT CONFLICT 338 338 T -> A (IN REF. 2 AND 3).
FT CONFLICT 342 342 R -> S (IN REF. 3).
FT CONFLICT 346 346 T -> N (IN REF. 3).
FT CONFLICT 376 376 V -> C (IN REF. 2 AND 3).
FT CONFLICT 526 527 WS -> RP (IN REF. 2).
FT CONFLICT 527 527 S -> P (IN REF. 2).
FT CONFLICT 535 535 D -> G (IN REF. 2 AND 3).
FT CONFLICT 535 535 D -> G (IN REF. 2 AND 3).
SQ SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;

Query Match 69.1%; Score 1866.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 1.6e-120;
Matches 320; Conservative 75; Mismatches 82; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLDNDGNHNRNLNSDASNLKSKITAWIPPAKKGASQNDVGYGAYDLYD 65
Db 39 NGTMMQYFEWYLDNDGNHNRNLNSDASNLKSKITAWIPPAKKGASQNDVGYGAYDLYD 98
Qy 66 LGSEFNQKGTVRTKYGRSOLQAQAAVTSILKNGIOVYGDVNMHKGADATEMRAVEVNP 125
Db 99 LGSEFNQKGTVRTKYGRSOLQAQAAVTSILKNGIOVYGDVNMHKGADATEMRAVEVNP 158
Qy 126 NRNQEVTEYTBIAWTRFDPPGRGNTHSSPKFWRYHFDGVDWDQSRRLNRIYKFRGHGK 185
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Db 159 DRNQEISGTQIQAWTFDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 AWDNEVDTEGNYDYLWYADIMDHPVYVNLWGWYVNTLGLDGFRIIDAVKHIXYSP 245
Db 218 AWDNEVDTEGNYDYLWYADIMDHPVYVNLWGWYVNTLGLDGFRIIDAVKHIXYSP 277
Qy 246 TRDINHVRATGKMFVAFWKNLGAENYLOKTNWHSVDFVPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNFYTASKSGG 337
Qy 306 NYDMNRTFNGTVVORHPHSHAVTFVDNHDSDPEEALSFVSEMEKPLAYALTLTREOGVPS 365
Db 338 TFDNRTLTMTNMDKQPTLAVTFVDNHDTEFCQALQSWDFWFLAYAFALTITKQSGIPC 397
Qy 366 VFYGDYGIPTGHPVPMARSKIDPLEARQKAYGQNDYLDHNNIIGTWREGTNAHPNSG 425
Db 398 VFYGDYGIPTGHPVPMARSKIDPLEARQKAYGQNDYLDHNNIIGTWREGTNAHPNSG 457
Qy 426 LATIMSGAGGSKWFGVGRNKGAGQWSDITGNRTGTVTINADGWNFSVNGSGSVSIW 483
Db 458 LAALITDGPGGKMYVKGQKAGKVFYDLTGNSDVTVTINSDBGWGEFKVNGSGSVVW 515

RESULT 4

AMY BACAM
ID - AMY BACAM STANDARD; PRT; 514 AA.
AC P00692;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1.4-alpha-D-glucan
glucanohydrolase).
OS Bacillus amyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IH;
RX MEDLINE=83108808; PubMed=6185474;
RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
Kaeeriaainen L.;
RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
deduced from the nucleotide sequence of the cloned gene.";
RL J. Biol. Chem. 258:1007-1013(1983).
RN [2]
RP SEQUENCE OF 32-222.
RX MEDLINE=80241725; PubMed=6156671;
RA Chung H.S., Friedberg F.;
RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
amylase.";
RL Biochem. J. 185:387-395(1980).
RN [3]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=82051296; PubMed=6170539;
RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
Soederlund H., Takkinen K., Kaeeriaainen L.;
RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
RL Gene 15:43-51(1981).
RN [4]
RP SEQUENCE OF 1-39 FROM N.A.
RX MEDLINE=88137952; PubMed=2830166;
RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karanen S.;
RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
its own signal peptide from Saccharomyces cerevisiae host cells.";
RL Gene 59:161-170(1987).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase."

High-resolution analysis of native and ligand complexes.";
Biochemistry 39:9099-9107(2000).
-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides
-1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
-1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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EMBL; J01542; AAA22191.1; -;
EMBL; V00092; CAA23430.1; -;
EMBL; A20154; CAA01489.1; -;
EMBL; M18424; AAA22192.1; -;
PIR; A92389; ALBSN.
PDB; 1E3X; 21-JUN-01.
PDB; 1E3Z; 24-JUN-03.
PDB; 1E40; 24-JUN-03.
PDB; 1E43; 21-JUN-01.
InterPro; IPR006589; Alp amyl cat sub.
InterPro; IPR006047; Alpha amyl cat.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
PRINTS; PR00110; ALPHAAMYLASE.
SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
Signal; 3D-structure.
FT SIGNAL 1 31 ALPHA-AMYLASE.
FT CHAIN 32 514
FT ACT SITE 262 262
FT ACT SITE 292 292
FT ACT SITE 359 359
FT METAL 133 133
FT METAL 190 190
FT METAL 212 212
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FT CONFLICT 84 84
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Query Match 67.9%; Score 1836; DB 1; Length 514;
Best Local Similarity 66.2%; Pred. No. 1.8e-118;
Matches 323; Conservative 64; Mismatches 93; Indels 8; Gaps 3;

Qy 3 NGTGTWQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGSQNDVGYGAYD 62
Db 30 SAVNGTLWQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGSQNDVGYGAYD 89
Qy 63 LYDLGEFNQKGTVRKTYGTRSQLQAAYVTSKNNNGIQYGVVMMHKGADATENVRAVEV 122
Db 90 LYDLGEFNQKGTVRKTYGTRSQLQAAYVTSKNNNGIQYGVVMMHKGADATENVRAVEV 149
Qy 123 NPNNRNEVTGEYTIETAWTFDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRG 182
Db 150 NPNNRNEVTGEYTIETAWTFDFPGRGNTYSSFKRWYHFDGVDWDSRKL-SRIYKFRG 208


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Db 421 AFSRSGTEENP--CCVVVLSNGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEAT 478
Qy 472 FSVNGGVSIVW 483
Db 479 FFCNAGSVSVW 490

RESULT 6
ID AMY2_ECOLI
AM2_AMY2_ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Jall;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12; MG1655;
RX MEDLINE=97251358; PubMed=9097040;
RA Icho T., Alba H., Baba T., Fujita K., Hayaashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=Jall;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=Jall;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIb, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L01642; AAA23810.1; -.
CC EMBL; AE000285; AAC74994.1; -.
CC EMBL; D90833; BAA15755.1; -.
CC EMBL; M85240; -; NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; -.
CC PIR; D64956; A45738.
CC HSP; P06278; 1VUS.
CC Ecogene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC CONFLICT 19 20 KL -> SS (IN REF. 1).
CC CONFLICT 109 109 A -> V (IN REF. 1).
CC CONFLICT 149 149 Q -> E (IN REF. 1).
CC CONFLICT 234 234 L -> I (IN REF. 1).
CC SEQUENCE 495 AA; 56639 MW; 2eAFF6797DDA54D6 CRC64;
Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAKMGASQN-DVVGADVLY 64
Db 3 NPTLLQCFHWYPEGGKLWPELAERADGPNIDGINWMLPPAYKSGSGVSDYDLF 62
Qy 65 DLGEFNKGVTQYKTRSOLOQAATVSLKNGQVGVGVVNMHKGADATWVRAVNP 124
Db 63 DLGEFDQKGSIPYKYGDKAQLAALDAIKRNDIAVLDDVVVNMHKGADAEKAIKRVQVNA 122
Qy 125 NNRNQEVTEGYTTEAATRFDPFGKGNTHSSFKRWYHFDGVDMDQSRRLNRIYKFRGH- 183
Db 123 DDRQTIDEEIIECEGWTRYTFPARAGQYSQFIWDFKCFSGIDHIENPD-EDGIFKIVNDY 181
Qy 184 -GKAWDEVTENGNDYLYADIMDPHPEVFNELRNWGVYNTLTGLDGRIDAVKHK 242
Db 182 TGEWNDQVDDELGNFDYLMGENIDFRNHAATEIKYARWVMBQTCDCGFRLDVAKHIP 241
Qy 243 YSFTRDMNHVRSATGKNMFAVEAFKNDLGAENLQKTNHNSVDFVPLHLYNLYASK 302
Db 242 AMFYKEWIEHVQEVAPKPLFVAVYNSHSDKLTQYIDQVEGKTMFLDPAQMKFHEASR 301
Qy 303 SGGNYDMRNIFNGTVQVORHPSHAVTVFDNHDSDPEEALESFVEBWKPLAYALTLTREOG 362
Db 302 MGRDYMTQITPTGLVEADPFHATLVANHDTPQLQALEAPVEPWFPLAYALLIRENG 361
Qy 363 YPSVFGDYGYGIPTHGVPA-----MRSKIDPILKQYKAYQKQNDYLDHNNIIG 412
Db 362 VPSVFPDLYGAHYEDVGGDGTVPIDMPIIEQLDELILARQFAHQVQTLFFDPHNCIA 421
Qy 413 WTRGNTAHNPSGLATITMSDAGGSKMFMVGRNKGQVSDITGNRTGTVTINADGWNF 472
Db 422 FSRSGTDEFP--GCVVMSNGDDGKTKLLGDNVANKTWKTRDFLGNRDEYVVTNDQGEATF 479

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Query Match 38.7%; Score 1045; DB 1; Length 495;
 Best Local Similarity 42.6%; Pred. No. 2.3e-64;
 Matches 209; Conservative 74; Mismatches 192; Indels 16; Gaps 5;

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QY 473 SVNGSVSIWV 483
Db 480 FCNGSVSVWV 490

RESULT 7
ID AMVB PAEPO STANDARD; PRT; 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [inclusion: Beta-amylase (EC 3.2.1.2)];
DE Alpha-amylase (EC 3.2.1.1).
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2];
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3];
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4];
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; M15817; AAA85446.1; -.
CC EMBL; Y00150; CAA68344.1; -.

DR PIR; A29130; A29130.
DR HSSP; P36924; 1B9Z.
DR InterPro; IPR006589; Alp_amyI_cat_sub.
DR InterPro; IPR006048; Alpha_amyI_C_cat.
DR InterPro; IPR006047; Alpha_amyI_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF03423; CBM_25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRINTS; PR00750; BETAAMYLASE.
DR SMART; SM00642; Amyy; 1.
DR SMART; SM00632; Amyy_C; 1.
DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196
FT DISULFID 118 126
FT ACT_SITE 198 198
FT ACT_SITE 394 394
FT MUTAGEN 118 118
FT MUTAGEN 126 126
FT MUTAGEN 358 358
FT CONFLICT 1 1
FT CONFLICT 67 67
FT CONFLICT 100 100
FT CONFLICT 154 154
FT CONFLICT 177 177
FT CONFLICT 227 228
FT CONFLICT 330 330
FT CONFLICT 425 425
FT CONFLICT 493 493
FT CONFLICT 532 532
FT CONFLICT 559 559
FT CONFLICT 665 665
FT CONFLICT 681 681
FT CONFLICT 686 686
FT CONFLICT 725 728
FT CONFLICT 736 736
FT CONFLICT 741 741
FT CONFLICT 758 758
FT CONFLICT 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;
SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;

Query Match 12.2%; Score 331; DB 1; Length 1196;
Best Local Similarity 23.7%; Pred. No. 5e-15; Indels 138; Gaps 24;
Matches 123; Conservative 70; Mismatches 188;

QY 1 HINGTGTWQVPEWYLPNDGNHNRNLSNDSALSKSGITAVWIPPAWKASQNDV-GYG 59
Db 766 NYGGFNNSDQRKWH-----GGDFQGIINKLDYIKMGTAIWITPTMCKSEVAYHGYH 821
QY 60 AYDLYDLGFEFNQKGTVRTKYGTRSQAAVTSLKNGIQYGVGVNHHKGGADATEMVR 119
Db 822 TYDFY-----AVDGLHGTMDKLQELVRKAHDKNIAVMVDVNVNHTG----- 862
QY 120 VEVPNNRQEVGTETIAWTFPDF-PGRGNTHSSP-KRWYVHFGVDWDQSRNNRI 177
Db 863 -----DFQPGNGFAKAPFDKADWYHHNGDITDGDYNSNNQ- 897
QY 178 YKFRGHGKAWDMVDVTENGNDYDLYMTADIDMDHPEVNVNELRNWGVVYNTLTGLDGRIDA 237
Db 898 -----WKI--ENG--DVAGLDDLHNENPATANELKWKILLNETGIDGLRLDT 942
QY 238 VKHIKYSFTRDWINHVRSATGKRMFAVEFWKNDLGAENLYLQKTNWHSVDFVPLHYNL 297

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Db 943 VKHVPKFLKDF-----DQANFTTWEIIPHGDPAVYGDY---TRYLDAALDFPMYTI 993
QY 298 YNASKSGGNDMRNIFNGTVVQHPHSHAVT---FVDNHDSPQEEALSFF-----344
Db 994 KDV--FGHQDSMRKIDRYDRQATNGVFDNHD-----VRFNDASGKPGAN 1045
QY 345 -EWFK-PLAYALTLTREOQVPSVYGDYGIPTGHPVPMRSKIDPILAEARQKAYGKON 402
Db 1046 YDKWPQLKAALGFTLT-SRGIPITIQTEQYSGGDDPANRENN-----FNANH 1094
QY 403 DYLDHNNIIGTWRENTAHNSGLATIMSDGAGSKWM-----FVGRNKAG-----Q. 449
Db 1095 DLVQYIAKLNVRRN---HP-----ALQNGSQREKWKVDSDSFYSFQSKNGKDEAIVFINN 1145
QY 450 VMSDIT---GN-----RTGTVTINADGWNFSVNGGVSU 481
Db 1146 SWSQTFITGNFNLNSGTLTNQLSNDSVQINNGSITV 1184

RESULT 8
AMYA VIGMU STANDARD; PRT; 421 AA.
ID AMYA VIGMU STANDARD; PRT; 421 AA.
AC P17859;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (Black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RT "Nucleotide sequence of cDNA for alpha-amylase from cotyledons of
RT germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RT "Nucleotide sequence of the alpha-amylase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC -----
CC EMBL; X53049; CAA37217.1; --
CC EMBL; X73301; CAA51734.1; --
CC PIR; S10514; S10514.
CC HSSP; P04063; IAVA.
CC InterPro; IPR006589; Alp amyl cat sub.
CC InterPro; IPR006047; Alpha amyl cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.

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KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT CHAIN 1 23 PROBABLE.
FT ACT_SITE 24 421 ALPHA-AMYLASE.
FT ACT_SITE 201 309 BY SIMILARITY.
FT METAL 113 113 BY SIMILARITY.
FT METAL 130 130 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 135 135 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 149 149 CALCIUM 3 (BY SIMILARITY).
FT METAL 160 160 CALCIUM 3 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 170 170 SIMILARITY).
SQ SEQUENCE 421 AA; 46888 MW; 15CA0DABA3DB4656 CRC64;

Query Match 10.4%; Score 281.5; DB 1; Length 421;
Best Local Similarity 25.3%; Pred. No. 3.4e-12;
Matches 98; Conservative 56; Mismatches 144; Indels 89; Gaps 15;

QY 9 MMQYFEWYLPNDGNHNRINLNSDASNLKSGITAVWIPPAKMGASQNDVGYCAYDLYDGE 68
Db 26 LFQGFNWESSKGGWYNSLKNISIPDLANAGITHYWLPPPSQSVSPR--GYLPGLYDLD- 82
QY 69 FNQKGTVRTKYTRSLQAAVTSLNKNGIOVYGDVVMNHKGADATEWRAVEVNPNNRN 128
Db 83 -----ASKYGSKNELSLIAAFHEKGIKCLADIVINHR-----TAER 119
QY 129 QEVGYTIEAWTRFDPPFGRGNTHSSPKRWYHFDGVDWDQSRRLNRIYKFRGHGKAWD 188
Db 120 KDGRIYCI-----FE-----GGTPDSRQ-----DWGSPFCRD-----D 149
QY 189 WEVDTEGNYD-----YLMYADIDMDHPEVNVNENLNGWYNTVTLGLDGFIDAVKHLYS 244
Db 150 TAYSDGTGNNDSGEGYDAAPDIDHLNFOVRELSEMMNWLKTEIGFGWRFDFVKGAPS 209
QY 245 FTRDWINHVRSATGKNMFVAEFW-----KNDLCAIENLYQKTNWNSVF 289
Db 210 ISKIYMEQT-----KPDFAVGEKWDSSISYQDGKPNYQDSHRGALVNWESAGAITAF 264
QY 290 DVPLHLYNLNASKSGGNYDMRNIFNGT---VVRHPSHAVTFFVDNHDSPQEEALSFF-VE 345
Db 265 DFTTK-GILQAAVQGLWRLIDP-NGKPPGMIGVKPENAVTFIDNHDGTGRLWLPFSD 322
QY 346 EWFKPLAYALTLTREOQVPSVYGDY 372
Db 323 KVMQGVAYILT---HPGTPSIFYDHF 346

RESULT 9
AM3A ORYSA STANDARD; PRT; 440 AA.
ID AM3A ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE Glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amylase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).

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FT METAL 153 163 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 168 168 SIMILARITY).
FT METAL 169 169 CALCIUM 1 (BY SIMILARITY).
FT METAL 172 172 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48637 MW; BD304250B40C7A8B CRC64;

Query Match 9.8%; Score 265; DB 1; Length 437;
Best Local Similarity 23.7%; Pred. No. 4.9e-11;
Matches 109; Conservative 57; Mismatches 155; Indels 138; Gaps 21;

Oy 9 MMQYFEWYLPN-DGNHNRNLSNDSNLKSGITAVWIPPAWKASONDVGAYDLYDLG 67
Db 29 LFOGFNWSWKQGGWYNFLSHVDYIAATGVTHVWLPSPSHVAPQ--GYMPGRLYDL 86
Oy 68 EFNQKGTVRTKYGRSOLQAQAVTSLKNGNIOQYGVVNNHKGADATEMVRVAVNPNR 127
Db 87 -----ASKYGTGAELSLIAAFHSKSIKCVADIVINHR-CAD----- 122
Oy 128 NOEVTGYTTEAWTRFPFGNTHSSFKWYHFDGVDW---DQSRRLNNRIYKFRGHG 184
Db 123 YKDSRGYICI-----PEG-GTPDSRLDW-----GPDMTCSDDTQYSNG--RGH- 162
Oy 185 KAWDEVDTENGNYDYLMYADIDMDHPVNNELRWGWYNTLGLDFRIDAVKHYS 244
Db 163 -----RTGADFGAAPDIDLHNTVQELSDWLNWLSKVDGFWRLDFAKGYSAT 213
Oy 245 FTRDWINHVSATGNMFAVAFWKN-----DLGAIENYLOKTNWHSVF 289
Db 214 VAKTYVDNTPS-----FVVAEISNRYDNGNBPNSQDGRQELYNWAAVGPASAF 268
Oy 290 DVPLHNYLNASKGNGVDMNINFGT---VVQRHPSHAVTFVNDHDSQPEALESF-VE 345
Db 269 DFTTKGEL-QAAVQELWRMD-GNGKAPGMIGLPEKAVTFIDNHDGTSTGNSWPPPSD 326
Oy 346 ENFKPLAYALTIREQGPSYFYGDYGIPTGVPMARSKIDPILBARQYAKQNDYL 405
Db 327 KMQRAYAYILT---HPGVPCIFY----- 346
Oy 406 DHNNIIGW-----TREGNTAHNSGLATIMSDG 433
Db 347 DH--VFDWNLKQEIISTLAAVSRNGIHPGSKNIIAADG 383

RESULT 11
AM3B ORYSA
ID AM3B ORYSA STANDARD; PRT; 438 AA.
AC P27937;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AM1.6 OR AMY3B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RL "Characterization of an alpha-amylase multigene cluster in rice.";
RN Plant Mol. Biol. 16:579-591 (1991).
RP [2]
SEQUENCE FROM N.A.

```

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RA Sutliff T.D., Huang N., Rodriguez R.L.;
RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Germinating seeds.
CC -!- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; X56337; CAA39777.1; -.
CC EMBL; M24941; AAA33897.1; -.
CC PIR; S14957; S14957.
CC HSSP; P04063; IAVA.
CC Gramene; P27937; -.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 438
FT ACT_SITE 205 205 ALPHA-AMYLASE ISOZYME 3B.
FT ACT_SITE 313 313 BY SIMILARITY.
FT METAL 117 117 BY SIMILARITY.
FT METAL 134 134 CALCIUM 1 (BY SIMILARITY).
FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
FT METAL 143 143 CALCIUM 2 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
FT METAL 168 168 SIMILARITY).
FT METAL 169 169 CALCIUM 1 (BY SIMILARITY).
FT METAL 172 172 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 48591 MW; B9DE0DB5ABC63F9C CRC64;

Query Match 9.8%; Score 265; DB 1; Length 438;
Best Local Similarity 23.5%; Pred. No. 4.9e-11;
Matches 109; Conservative 55; Mismatches 153; Indels 146; Gaps 22;

Oy 9 MMQYFEWYLPN-DGNHNRNLSNDSNLKSGITAVWIPPAWKASONDVGAYDLYDLG 67
Db 29 LFOGFNWSWKQGGWYNFLSHVDYIAATGVTHVWLPSPSHVAPQ--GYMPGRLYDL 86
Oy 68 EFNQKGTVRTKYGRSOLQAQAVTSLKNGNIOQYGVVNNHKGADATEMVRVAVNPNR 127
Db 87 -----ASKYGTGAELSLIAAFHSKSIKCVADIVINHR-CAD----- 122
Oy 128 NOEVTGYTTEAWTRFPFGNTHSSFKWYHFDGVDW---DQSRRLNNRIYKFRGHG 184
Db 123 YKDSRGYICI-----PEG-GTPDSRLDW-----GPDMTCSDDTQYSNG--RGH- 162
Oy 185 KAWDEVDTENGNYDYLMYADIDMDHPVNNELRWGWYNTLGLDFRIDAVKHYS 244

```

Db 163 -----RDTGADGAAPDIDHLNTRVQTELSLWNLKSDVGFDFGRLDFAGYSAA 213
Qy 245 FTRDWINHVSATGKNMFAVAEFWKN-----DLGATENYLQKTNHNSVF 289
Db 214 VAKTYVDNTDPS-----FVVAEISWNRVYDNGEPEPSWNQDGRQELVNNWAQVGGPASAF 268
Qy 290 DVPLHNLNYSKSGNGYDMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEEALSFVEE 346
Db 269 DFTTKGEL-QAAVQGLWRMKD-GNGKAPGCMIGWPEKAVTFIDNHD-----GSTQNS 320
Qy 347 WFKP-----LAYALTLTREGYPSVFGYDYGITPGVPMRSKIDPILBAROKYAYGKQ 401
Db 321 WPPFSKVMQGYAYILT-HPGVPCIFY----- 346
Qy 402 NDYLDHNNIGW-----TREGNTAHPNSGLATIMSDG 433
Db 347 -----DH--VFDWNLKQBISTIAVRSRNEIHPGSKLKILAREG 383

RESULT 12

AM3D ORYSA
ID AM3D ORYSA STANDARD; PRT; 435 AA.
AC P27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etisolated leaf;
RX MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reinl S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes";
RL Nucleic Acids Res. 18:7007-7014 (1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
clones and mRNA expression during seed germination";
RL Mol. Gen. Genet. 221:235-244 (1990).
CC -|- FUNCTION: Important for breakdown of endosperm starch during
germination.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -|- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -|- SUBUNIT: Monomer.
CC -|- TISSUE SPECIFICITY: Is expressed in all tissues, except in
immature seeds. Is the most abundant alpha-amylase isozyme in
callus.
CC -|- DEVELOPMENTAL STAGE: Expressed at a high level during germination
in the aleurones cells under the control of the plant hormone
gibberellic acid and in the developing grains at a low level.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M59351; AAA33895.1; -.
DR EMBL; M24287; AAA33886.1; -.
DR PIR; S12625; S12625.
DR HSSP; P04063; 1A1A.
DR Gramene; P27933; -.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 435
FT ACT_SITE 203 203
FT ACT_SITE 311 311
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
FT CONFLICT 73 74
FT CONFLICT 137 137
SQ SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;
Query Match 9.8%; Score 264.5; DB 1; Length 435;
Best Local Similarity 25.6%; Pred. No. 5.2e-11;
Matches 100; Conservative 50; Mismatches 150; Indels 91; Gaps 19;
Qy 2 HNGTNGTMMQYFEW-YLPNDGNHNRNLNSDASMLKSGITAVWIPPAWKGASNDVGYGA 60
Db 21 NSGQAQVLFQGFNWSWKQGGWYNNLKGQVDDIAKAGVTHVWLPSPSHVAPQ--GYMP 78
Qy 61 YDIYDLGEGFNQKGTVTYKTSQQAATSLKNGNGIOVGVVMMHKGADATMVRVAV 120
Db 79 GRLYDLD-----ASKYGTAAELKSLTAAFHGKGVQCVADVVIH-----RCA 120
Qy 121 EVNPNRNRQEVTEGYTIEAWTRDFPFGNGNTHSSFKRWYHFDGVQDQSRRLNRIYKF 180
Db 121 E-----KKDARGVYCV-----PE-----GGTP-----DRLDWGPGMICSDDTQYS 155
Qy 181 RGHGKAWDEVDTEGNGYDLYMYADIDMDHPEVNVNLRWGVVYTYTLGLDGRIDAVKH 240
Db 156 DGTGHR-----DTGEG---FGAAPDIDHLNPRVQRELTDLNWLKSDVGFDFGRLDFAGK 207
Qy 241 IKYSFTFDWINHVSATGKNMFAVAEFWKN-----DLGAIENYLQKTNHNS 287
Db 208 YSTDIAMKYVESCKPG-----FVVAEISWNLKSGNGYDMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEE 338
Qy 288 V-----FDVPLHNLNYSKSGNGYDMRNIFNGT---VVQRHPSHAVTFVDNHDSDQPEE 338
Db 259 VGGPAMTFFTTK-GLLQAGVQGLWRMKD-GNGKAPGCMIGWPEKAVTFIDNHDGTSQ 316
Qy 339 ALESP-VEEWFKPLAYALTLTREGYPSVFPY 368
Db 317 KLWPPPSDKVMQGYAYILT-HPGVPCIFY 344
RESULT 13
AMT4 PSESA
ID AMT4 PSESA STANDARD; PRT; 551 AA.
AC P22963;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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 EMBL; K02638; AAA32933.1; --
 DR HSP; P04063; IAVA.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR PRINTS; PR00110; ALPHARAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
 KW Calcium-binding; Signal; Multigene family.
 FT SIGNAL 1 24
 FT CHAIN 25 >368 ALPHA-AMYLASE TYPE B ISOZYME.
 FT ACT_SITE 203 BY SIMILARITY.
 FT ACT_SITE 228 BY SIMILARITY.
 FT ACT_SITE 313 BY SIMILARITY.
 FT METAL 115 CALCIUM 1 (BY SIMILARITY).
 FT METAL 132 CALCIUM 2 (BY SIMILARITY).
 FT METAL 135 CALCIUM 2 (BY SIMILARITY).
 FT METAL 137 CALCIUM 2 (BY SIMILARITY).
 FT METAL 141 CALCIUM 2 (BY SIMILARITY).
 FT METAL 151 CALCIUM 3 (BY SIMILARITY).
 FT METAL 162 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT METAL 165 SIMILARITY).
 FT METAL 166 CALCIUM 1 (BY SIMILARITY).
 FT METAL 167 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT METAL 170 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT METAL 172 CALCIUM 1 AND 3 (BY SIMILARITY).
 FT METAL 368
 FT NON_TER 368
 SQ SEQUENCE 368 AA; 40787 MW; A237EF55793BA93B CRC64;
 Query Match 9.6%; Score 260; DB 1; Length 368;
 Best Local Similarity 24.3%; Pred. No. 8.6e-11;
 Matches 101; Conservative 59; Mismatches 148; Indels 108; Gaps 18;
 Qy 9 MMQYFEW-YLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGASQNDVGYDLYDLG 67
 Db 27 LFQGFNWSKNGGWTFNLMGKYDDIAAAGITHVWLPASQSAEQ--GYMFGRLYDLD 84
 Qy 68 EFNQKGVTRKYGRSLOAAVTSLNKNGIQVYDVVMHKGADATEMVRVAVNPNNR 127
 Db 85 -----ASKYGNKAQLKSLIGHKGKGVKATADIVNHR----- 117
 Qy 128 NQEVGTYYTTEAWTRDFPGRGNTSHSFKRWYHFDGV-----DWDQSRRLANNRYKFR 181
 Db 118 -----TAEHK-----DGRG-----IYCFEGVTPDARLDWGHMFCRDRPYAD 156
 Qy 182 GHGKAWDEVDTENGNYDLYMADI DMHPVEVNLNNGWYNTLGLDGFRLDAVKHI 241
 Db 157 GTGNP-----DT-----GADFGAAPDHLNLRVQKELAEWLNWKADTGFDFGWRPFAKY 208
 Qy 242 KYSTFRDWINHVRSATCKNMFVAEWF-----KNDLGATENYQKTNWHSV----- 288
 Db 209 SADVAKIYIDR-----SEPSFAVAEITWISLAYGDDGPNLNQDHRRELNVWVDKVGKG 263
 Qy 289 -----FDVPLHYNLNASKSGNYDMRNIFNGT-----VVQRHPSHATVFDNHDSOPEE 338
 Db 264 PATTFDPTTK-GILNVAVEGLWRLR-----GTDGKAPGMIGWMPAKAVTFVDNHDGTSTQ 318
 Qy 339 ALESF-VVEWPKPLAYALTLTREOGYPSVFYGYGPIPTHGVPAMRSKIDPILLEAR 393
 Db 319 HMPFPSPDRVMQGYAYILT---HPGTPCIFYDFHFDW-----GLKEIDRLVSVR 365

RESULT 15
 AMT4_PSEST STANDARD; PRT; 548 AA.
 AC FI3507;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-
 DE amylase) (Maltotetraose-forming amylase) (Exo-maltotetraohydrolase)
 DE (Maltotetraose-forming exo-amylase).
 GN AMYP.
 OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=316;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=MO-19;
 RX MEDLINE=89155431; PubMed=2646279;
 RA Fujita M., Torigoe K., Nakada T., Tsusaki K., Kubota M., Sakai S.,
 RA Tsujisaka Y.;
 RT "Cloning and nucleotide sequence of the gene (amyP) for
 RT maltotetraose-forming amylase from Pseudomonas stutzeri MO-19.";
 RL J. Bacteriol. 171:1333-1339(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 286-302.
 RC STRAIN=MO-19;
 RX MEDLINE=97271999; PubMed=9126844;
 RA Morishita Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.,
 RA Sakai S.;
 RT "Crystal structure of a maltotetraose-forming exo-amylase from
 RT Pseudomonas stutzeri.";
 RL J. Mol. Biol. 267:661-672(1997).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF VARIANT GLN-240.
 RC STRAIN=MO-19;
 RX MEDLINE=97428332; PubMed=9281429;
 RA Yoshioka Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;
 RT "Crystal structures of a mutant maltotetraose-forming exo-amylase
 RT cocrystallized with maltopentaose.";
 RL J. Mol. Biol. 271:619-628(1997).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF VARIANTS.
 RC STRAIN=MO-19;
 RX MEDLINE=20027472; PubMed=10556241;
 RA Hasegawa K., Kubota M., Matsuura Y.;
 RT "Roles of catalytic residues in alpha-amylases as evidenced by the
 RT structures of the product-complexed mutants of a maltotetraose-forming
 RT amylase.";
 RL Protein Eng. 12:819-824(1999).
 CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amylaceous polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -I- COFACTOR: Binds 2 calcium ions per subunit.
 CC -I- PATHWAY: Starch degradation.
 CC -I- SUBUNIT: Monomer.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- MISCELLANEOUS: THERE ARE SEVERAL ISOENZYME FORMS OF THIS PROTEIN.
 CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M24516; AAA25707.1; --
 DR PUR; A32803; A32803.
 DR PDB; 1GCV; 28-JAN-03.

PDB; LJDA; 15-OCT-97.
PDB; LJDC; 15-OCT-97.
PDB; LJDD; 15-OCT-97.
PDB; IQI3; 24-NOV-99.
PDB; IQI4; 24-NOV-99.
PDB; IQI5; 24-NOV-99.
PDB; IQPK; 17-NOV-99.
PDB; 2AMG; 01-APR-97.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR006046; Glyco_hydro_13.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00686; CBM_20; 1.
PRINTS; PR00110; ALPHAMYLASE.
ProDom; PD001568; CBD_4; 1.
Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 548
FT ACT_SITE 214 214
FT ACT_SITE 240 240
FT ACT_SITE 315 315
FT METAL 22 22
FT METAL 23 23
FT METAL 34 34
FT METAL 37 37
FT METAL 38 38
FT METAL 137 137
FT METAL 172 172
FT METAL 175 175
FT METAL 183 183
FT METAL 218 218
FT DISULFID 161 171
FT DISULFID 237 272
FT CONFLICT 286 302
GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.
CALCIUM 2.
CALCIUM 2 (VIA CARBONYL OXYGEN).
CALCIUM 2.
CALCIUM 2.
CALCIUM 2.
CALCIUM 1.
CALCIUM 1.
CALCIUM 1 (VIA CARBONYL OXYGEN).
CALCIUM 1.
CALCIUM 1 (VIA CARBONYL OXYGEN).
GSIADWKHGLNGNDPDR -> ARSPTGSTPERQSRPA (IN REF. 1).
FT TURN 28 29
FT TURN 34 35
FT STRAND 40 42
FT TURN 46 47
FT HELIX 48 51
FT TURN 53 55
FT HELIX 56 62
FT TURN 63 63
FT HELIX 64 69
FT TURN 70 71
FT STRAND 74 77
FT STRAND 87 89
FT TURN 90 91
FT STRAND 92 94
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FT STRAND 108 108
FT TURN 109 110
FT STRAND 111 111
FT HELIX 113 126
FT TURN 127 127
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FT TURN 271 271
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FT HELIX 363 376
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FT STRAND 383 387
FT STRAND 393 398
FT STRAND 403 408
FT HELIX 415 417
FT TURN 418 418
FT STRAND 424 429
FT TURN 430 433
FT STRAND 434 438
SQ SEQUENCE 548 AA; 59876 MW; 2B87217B3379158F CRC64;
Query Match 9.6%; Score 259; DB 1; Length 548;
Best Local Similarity 23.6%; Pred. No. 1.6e-10;
Matches 124; Conservative 68; Mismatches 168; Indels 166; Gaps 26;
QY 2 HNGTNGTMMQVFEWYL-----PNDGNHNRLNSDASNLKSGKITAVWIPPAWKASQNDVVG 57
DB 33 YHGGDEILLOGFHWNVREAPND--WYNILRQARTTAADGFSAIWMPFVWRDFSSWSDG 90
QY 58 --YGAYDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLKNGINGIQYGVVMNH--KGGADA 113
DB 91 SKSGGGEYFWDHFNKNG---RYGSDAQLRQAASALGGAGVKLYDVPVHNRRGYDDK 146
QY 114 TEMVRAVEVN--PNNRNOEVTGEYITIAWTRFDPGRGNTSSFKRWYHFDGVNDQSR 172
DB 147 -----EINLPAG-----QGFWRNDCADPGN-----YPNDCDDG----- 175
QY 173 LNNRIYKFRGHKAWDWEVDTENGNYDLYMAYADIMDHDPVNNELRNWGVVYNTLGLDG 232
DB 176 -----RFIG-----ADLNTGHPQVYGMFRDEFNLSQYAGG 210
QY 233 FRIDAVKHIKYSFTRDWINHVRSATGKNMFAVAFWKNDLGAIE---NYLQKTNNH-- 286
DB 211 FRDFVR---GYAPERVNSWMTDSADNSFCVGLWK---GPSEYPNWDWRNTASWQII 263
QY 287 -----SVFDVPLHYNLYNASKSGNVDNRNIFNGTVVQRHPSHAVTFVDNHDSDPE 337
DB 264 KWSMDRAKCPVDFPFALKERMONGSIA---DWKHGLNGNDPDRWREVAVTFVDNHDGYS 319
QY 338 BALESFVEW-----FKPLAYALTIREQYPSVF-----YGDYGGIPTHGVPMRS 384
DB 320 PGQNGGQHHLAQDGLIRQAYILT--SPGTVPVYWSHMYDWGYGDF----- 365
QY 385 KIDPILFAROKYAYKQNDYLDHNNIIGWTRREGNTAHPNSGLATIMSDGAGGSKWPFVGR 444
DB 366 -IRQLIQVRR--AAG-----VRASATSFHSGYGLVATVSGSQOTLVVAL 408
QY 445 N-----KAGQVSWDITGNRTCTVTINADGWGNFS-----VNGGSYSIW 482
DB 409 NSDLGNPQVAS-----GSFSEAVNASNGQVRVW 437

us-09-925-576c-13.rsp

Thu Oct 7 08:31:55 2004

Search completed: October 7, 2004, 00:13:27
Job time : 10.5063 secs


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QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
DB 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
QY 361 QGYPSPFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSPFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485
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RESULT 2

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US-09-170-670-6
; Sequence 6, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-6
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Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
DB 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
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QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
QY 361 QGYPSPFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSPFYGDYIGIPTHGVPAMRSKIDPILBARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485
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RESULT 3

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US-09-193-068-6
; Sequence 6, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-6
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Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGDVVMNKHGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
DB 121 EVNPNRNRQEVGTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWQSRRLNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTEGNGYDYLMDHPEVNNELRNWGWYNTTILGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLQKTNWNHVSFVDPPLHYNLYNA 300
QY 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRNI FNGTVVQRHPSHVAFTVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
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QY 361 QGYSVFGYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYSVFGYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMEVGRNKAGQVMSDITGNRTGTTINADGWGNFVNGGVS 480
DB 421 HPNSGLATIMSDGAGGSKWMEVGRNKAGQVMSDITGNRTGTTINADGWGNFVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 4

US-09-183-412-6
; Sequence 6, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-6

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
QY 61 YDLGLGEFQKGTVRTKGYTRSQLAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLGLGEFQKGTVRTKGYTRSQLAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNEQVTEGTYTTEAWTRFDPGGRNTHSSFKWRWYHFDGVDQSRLLNNRIYKF 180
DB 121 EVNPNRNEQVTEGTYTTEAWTRFDPGGRNTHSSFKWRWYHFDGVDQSRLLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNYDYLWADIOMDHPVNVNLRNMGVWYTNLTGLDGFDAVKH 240
DB 181 RGHGKAWDEVDTEGNYDYLWADIOMDHPVNVNLRNMGVWYTNLTGLDGFDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNFAVAEFKNDLGAENYLOKTNWHSVDFVPLHNLNYA 300
DB 241 IKYSFTRDWINHVRSAATGKNFAVAEFKNDLGAENYLOKTNWHSVDFVPLHNLNYA 300
QY 301 SKSGGNYDMENIENGTVVQRHPSHAVTFVNDHDSQPEEALESFVEEFKPLAYALTRE 360
DB 301 SKSGGNYDMENIENGTVVQRHPSHAVTFVNDHDSQPEEALESFVEEFKPLAYALTRE 360

QY 361 QGYSVFGYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYSVFGYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKWMEVGRNKAGQVMSDITGNRTGTTINADGWGNFVNGGVS 480
DB 421 HPNSGLATIMSDGAGGSKWMEVGRNKAGQVMSDITGNRTGTTINADGWGNFVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 5

US-09-354-191A-7
; Sequence 7, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-354-191A-7

Query Match 100.0%; Score 2703; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWTPPAWKASQNDVGGA 60
QY 61 YDLGLGEFQKGTVRTKGYTRSQLAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLGLGEFQKGTVRTKGYTRSQLAAVTSKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNEQVTEGTYTTEAWTRFDPGGRNTHSSFKWRWYHFDGVDQSRLLNNRIYKF 180
DB 121 EVNPNRNEQVTEGTYTTEAWTRFDPGGRNTHSSFKWRWYHFDGVDQSRLLNNRIYKF 180

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QY 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
DB 421 HNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 6
US-09-291-023A-13
; Sequence 13, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Activity And Nucleic
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291.023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-13

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLVDLGEFNGKQGTVRTKGYTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLVDLGEFNGKQGTVRTKGYTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTIETAWTRFPDGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVGTGEYTIETAWTRFPDGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
QY 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
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DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
DB 421 HNSGLATIMSDGAGGSKWMFVGRNKGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 7
US-09-290-734-6
; Sequence 6, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Prantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-6

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223; Indels 0; Gaps 0;
Matches 485; Conservative 0; Mismatches 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLVDLGEFNGKQGTVRTKGYTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLVDLGEFNGKQGTVRTKGYTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVGTGEYTIETAWTRFPDGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
DB 121 EVNPNRNRQEVGTGEYTIETAWTRFPDGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
QY 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
DB 181 RHGKAWDEVDTEGNGYDYLMDYADIMDHPEVNNELRNWGVYTWTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNLDGAIENYLQKTNWNSHVSFVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
DB 301 SKSGGNYDMRNIFNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEWFKPLAYALTRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPMARSKIDPILFARQKAYAGKQNDYLDHNNIIGWTREGNTA 420
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Db 361 QGYPVFGYDYGIPTHGVPMRSKIDPILAEARQKAYKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485

RESULT 8
US-09-381-687-5
; Sequence 5, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-011SP
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp. #707
US-09-381-687-5

Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYDLGEFQKQVTRTKYGRSOLQAAVTSLNKNGIQVYGDVVVNNHKGADATEMVRV 120
Db 61 YDLYDLGEFQKQVTRTKYGRSOLQAAVTSLNKNGIQVYGDVVVNNHKGADATEMVRV 120
Qy 121 EVNPNRNQEVGTGEYTTIEAWTRDPFPGRNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYTTIEAWTRDPFPGRNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDLYMYADIMDHPVNVNLRNMGVWYTTNLGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDLYMYADIMDHPVNVNLRNMGVWYTTNLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNSHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNSHVSFVDFPLHYNLYNA 300
Qy 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPVFGYDYGIPTHGVPMRSKIDPILAEARQKAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGYDYGIPTHGVPMRSKIDPILAEARQKAYKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485

RESULT 10
US-09-540-715A-13
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Db 481 IWVNK 485

RESULT 9
US-09-545-586-6
; Sequence 6, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-6
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Query Match 100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYDLGEFQKQVTRTKYGRSOLQAAVTSLNKNGIQVYGDVVVNNHKGADATEMVRV 120
Db 61 YDLYDLGEFQKQVTRTKYGRSOLQAAVTSLNKNGIQVYGDVVVNNHKGADATEMVRV 120
Qy 121 EVNPNRNQEVGTGEYTTIEAWTRDPFPGRNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYTTIEAWTRDPFPGRNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDLYMYADIMDHPVNVNLRNMGVWYTTNLGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDLYMYADIMDHPVNVNLRNMGVWYTTNLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNSHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEPFKNDLGAENYLOKTNWNSHVSFVDFPLHYNLYNA 300
Qy 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGGNYDMENIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPVFGYDYGIPTHGVPMRSKIDPILAEARQKAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVFGYDYGIPTHGVPMRSKIDPILAEARQKAYKQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFGVRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGSVS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485
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; Sequence 13, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540,715A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-13

Query Match      100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60

QY 61 YDYLDFGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQYVGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDFGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQYVGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNRNQEVGTGEYTTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYTTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180

QY 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVAVNELRNWGVYNTLGLDGRIDAVKH 240
Db 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVAVNELRNWGVYNTLGLDGRIDAVKH 240

QY 241 IKYSFTRDWINHVRSATGKMFVAEFAWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKMFVAEFAWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300

QY 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTRE 360
Db 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTRE 360

QY 361 QGYPSVFYGYDYGIPTHGVPAMRSKIDPILFARQKYAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAMRSKIDPILFARQKYAYKQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 11
US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
```

```
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-6

Query Match      100.0%; Score 2703; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 4.7e-223;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKGASQNDVGYGA 60

QY 61 YDYLDFGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQYVGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDFGEFNQKGTVRTKYGTRSQLQAATVSLKNGIQYVGDVVMNHKGGADATEMVRV 120

QY 121 EVNPNRNQEVGTGEYTTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVGTGEYTTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180

QY 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVAVNELRNWGVYNTLGLDGRIDAVKH 240
Db 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVAVNELRNWGVYNTLGLDGRIDAVKH 240

QY 241 IKYSFTRDWINHVRSATGKMFVAEFAWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKMFVAEFAWKNDLGAENYLQKTNWHSVFDVPLHYNLYNA 300

QY 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTRE 360
Db 301 SKSGGNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTRE 360

QY 361 QGYPSVFYGYDYGIPTHGVPAMRSKIDPILFARQKYAYKQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAMRSKIDPILFARQKYAYKQNDYLDHNNIIGWTREGNTA 420

QY 421 HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSVS 480

QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 12
US-09-290-734-24
; Sequence 24, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Prantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
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NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-24

Query Match 96.7%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 2.3e-215;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVTIPPAWKGSQNDVGGA 60

Qy 61 YDLVLDGEFQKGTVRTKYGTRSQLOAAVTSKNGIQVYGVVNNHKGADATEMVRV 120
Db 61 YDLVLDGEFQKGTVRTKYGTRNQLOAAVNAKNSGQVYGVVNNHKGADATEMVRV 120

Qy 121 EVNPNRNRQEVGTTEATWTRFDPGGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVSGEYTTIEATWTKFDFPGGRGNTHSNFKRWYHFDGVDWQSRKLNNRIYKF 180

Qy 181 RGHGKANDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240

Qy 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLOKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300

Qy 301 SKSGNCDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360
Db 301 SKSGNCDMRQIFNGTVVQRHPMEAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILAEARKYAGKONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILAEARKYAGKONDYLDHNNIIGWTREGNTA 420

Qy 421 HPNSGLATIMSDGAGGSKMFPVGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFPVGRNKAGQVWTDITGNRAGTGTINADGWGNSVNGGSVS 480

Qy 481 IWVWK 485
Db 481 IWVWK 485
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RESULT 13

US-09-290-734-26
; Sequence 26, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Liabeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290.734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-26

Query Match 96.7%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 2.3e-215;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVTIPPAWKGSQNDVGGA 60

Qy 61 YDLVLDGEFQKGTVRTKYGTRSQLOAAVTSKNGIQVYGVVNNHKGADATEMVRV 120
Db 61 YDLVLDGEFQKGTVRTKYGTRNQLOAAVNAKNSGQVYGVVNNHKGADATEMVRV 120

Qy 121 EVNPNRNRQEVGTTEATWTRFDPGGRGNTHSSFKRWYHFDGVDWQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVSGEYTTIEATWTKFDFPGGRGNTHSNFKRWYHFDGVDWQSRKLNNRIYKF 180

Qy 181 RGHGKANDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNGYDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240

Qy 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLOKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEPWKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300

Qy 301 SKSGNCDMRNIFNGTVVQRHPSHAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360
Db 301 SKSGNCDMRQIFNGTVVQRHPMEAVTFVDNHDSPPEALESFVEEFKPLAYALTLTRE 360

Qy 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILAEARKYAGKONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFGYDYGIPTHGVPAKMSKIDPILAEARKYAGKONDYLDHNNIIGWTREGNTA 420

Qy 421 HPNSGLATIMSDGAGGSKMFPVGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFPVGRNKAGQVWTDITGNRAGTGTINADGWGNSVNGGSVS 480

Qy 481 IWVWK 485
Db 481 IWVWK 485
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RESULT 14

US-09-417-359A-5
; Sequence 5, Application US/09417359A
; Patent No. 6461849
; GENERAL INFORMATION:
; APPLICANT: Oleen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/09/417.359A
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-417-359A-5

Query Match 96.7%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 2.3e-215;

Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
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Db	1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVWIPPAWKAGSQNDVGGA 60
Qy	61 YDLYDLGEFNQKGTVRTKYGTRSQLAAVTSLKNGGIQVYGDVVMNHKGGADATEMVRV 120
Db	61 YDLYDLGEFNQKGTVRTKYGTRSQLAAVNAKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy	121 EVNPNRNQEVTEGYTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db	121 EVNPNRNQEVTEGYTIEAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy	181 RHGKAWDEVDTEGNYDYLMTADIDMDHPEVNVNELRWGWYNTLGLDGFRIIDAVKH 240
Db	181 RHGKAWDEVDTEGNYDYLMTADIDMDHPEVNVNELRWGWYNTLGLDGFRIIDAVKH 240
Qy	121 EVNPNRNQEVTEGYTIEAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db	121 EVNPNRNQEVTEGYTIEAWTKFDFPGRGNTHSNFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy	181 RHGKAWDEVDTEGNYDYLMTADIDMDHPEVNVNELRWGWYNTLGLDGFRIIDAVKH 240
Db	181 RHGKAWDEVDTEGNYDYLMTADIDMDHPEVNVNELRWGWYNTLGLDGFRIIDAVKH 240
Qy	241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLKTNMNHVSFVDPVPLHYNLYNA 300
Db	241 IKYSFTRDWINHVRSAATGKNMFAVAEFWKNDLGAENYLKTNMNHVSFVDPVPLHYNLYNA 300
Qy	301 SKSGGNYDMRNIIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Db	301 SKSGGNYDMRQIFNGTVVQRHPMHAFTFVDNHDSPQEEALESFVEEFKPLAYALTLTRE 360
Qy	361 QGYPSVFGDYGIPTGHPVPMRSKIDPILARQKYAYGQNDYLDHNNIIGWTREGNTA 420
Db	361 QGYPSVFGDYGIPTGHPVPMRSKIDPILARQKYAYGQNDYLDHNNIIGWTREGNTA 420
Qy	421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWNFSVNGGVS 480
Db	421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGGVS 480
Qy	481 IWVWK 485
Db	481 IWVWK 485

RESULT 15
US-09-545-586-24
; Sequence 24, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Prantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-24

Query Match 96.7%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 2.3e-215;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
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Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGISAVWIPPAWKAGSQNDVGGA 60

Search completed: October 7, 2004, 00:47:14
Job time : 16.0278 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-13

Perfect score: 2703

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGNGFVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2703	100.0	485	10	US-09-925-576C-13
5	2703	100.0	485	12	US-10-025-648-7
6	2703	100.0	485	12	US-10-025-648-7
7	2703	100.0	485	12	US-10-327-837-6
8	2703	100.0	485	16	US-10-477-725-13
9	2613	96.7	485	9	US-09-925-576C-12
10	2613	96.7	485	10	US-09-925-576C-12
11	2613	96.7	485	12	US-10-327-837-24
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13	2613	96.7	485	12	US-10-327-837-26
14	2613	96.7	485	14	US-10-209-812-5
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18	2440	90.3	485	9	US-09-769-864-7	Sequence 7, Appli
19	2440	90.3	485	9	US-09-854-346-2	Sequence 2, Appli
20	2440	90.3	485	9	US-09-902-188A-1	Sequence 1, Appli
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45	2410	89.2	516	9	US-09-971-611-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR FILING DATE: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-769-864-6

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	HHNGTGTMMQYFEWYLPNDGHNHNRINDASNLKSGITAVWIPPAWKASQNDVGYGA	60
QY	61	YDLYDLGEFNQKQTVTKYTRSQLAAVTSLNKNGIQVYGVVNMHKGADATEMVRV	120
Db	61	YDLYDLGEFNQKQTVTKYTRSQLAAVTSLNKNGIQVYGVVNMHKGADATEMVRV	120
QY	121	EVNPNRNEQVTEYTIETATWTRDFPGRGNTHSSFKWRVHFDGVDWDQSRLLNNRIYKF	180

Db 121 EVNPNRNQEVITGEYTI EAWTRFDFFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTENGNDYDLYMAYADIMDHPPEVVNELRWGVYNTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTENGNDYDLYMAYADIMDHPPEVVNELRWGVYNTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSATGKNMFAVAEFKNDLGAENYLQKTNWHSVDFVPLHYNLNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAEFKNDLGAENYLQKTNWHSVDFVPLHYNLNA 300
Qy 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEWFKPLAYALTLTRE 360
Db 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEWFKPLAYALTLTRE 360
Qy 361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILEARQKYAYGKQNDYLDHNNIIGWTRREGNTA 420
Db 361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILEARQKYAYGKQNDYLDHNNIIGWTRREGNTA 420
Qy 421 HNSGLATIMSDGAGGSKWFMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HNSGLATIMSDGAGGSKWFMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485

RESULT 2
US-09-854-346-13
; Sequence 13, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352AlcZymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus 707
; US-09-854-346-13

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
Db 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120
Qy 121 EVNPNRNQEVITGEYTI EAWTRFDFFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQEVITGEYTI EAWTRFDFFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy 181 RGHGKAWDEVDTENGNDYDLYMAYADIMDHPPEVVNELRWGVYNTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTENGNDYDLYMAYADIMDHPPEVVNELRWGVYNTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSATGKNMFAVAEFKNDLGAENYLQKTNWHSVDFVPLHYNLNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAEFKNDLGAENYLQKTNWHSVDFVPLHYNLNA 300

Qy 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEWFKPLAYALTLTRE 360
Db 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEWFKPLAYALTLTRE 360
Qy 361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILEARQKYAYGKQNDYLDHNNIIGWTRREGNTA 420
Db 361 QGYPSVFGDYIGIPTHGVPAMRSKIDPILEARQKYAYGKQNDYLDHNNIIGWTRREGNTA 420
Qy 421 HNSGLATIMSDGAGGSKWFMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Db 421 HNSGLATIMSDGAGGSKWFMFVGRNKAGQVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy 481 IWVNK 485
Db 481 IWVNK 485

RESULT 3
US-09-902-188A-7
; Sequence 7, Application US/09902188A
; Patent No. US20020098996A1
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; Svendsen, Allan
; Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. US20020098996A1o No. US20020098996A1disk of No. US20020098996A1
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/902,188A
; FILING DATE: 10-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/354,191
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4318.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-902-188A-7

Query Match 100.0%; Score 2703; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTVRTKYGTRSQLAAVTSLNKNGIQVYGVVMMHKGADATEMVRV 120

Db 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300
QY 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTRGNNTA 420
Db 361 QGYPSVFYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTRGNNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 4

US-09-925-576C-13
; Sequence 13, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: bacillus sp. 707
US-09-925-576C-13

Query Match 100.0%; Score 2703; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300

Db 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300
QY 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
QY 361 QGYPSVFYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTRGNNTA 420
Db 361 QGYPSVFYDYGIPHTGVPAMRSKIDPILFARQKAYGKQNDYLDHNNIIGWTRGNNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVMSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 5

US-10-665-667-6
; Sequence 6, Application US/10665667
; Publication No. US20040039368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; PRIOR FILING DATE: 2003-09-19
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 2001-01-25
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-665-667-6

Query Match 100.0%; Score 2703; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNQKGTVRTKYGTRSQLQAQAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
Db 121 EVNPNRNRQEVTEGTYTTEAWTRFDPGRGNTHSSFKRWYHFDGVDMDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMDADIMDHPEVNVNELRNKGVWYTNLTGLDGFPRIDAVKH 240
QY 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHRSATGKMFVAEAFWKNDLGAENYLOKTNWNHSHVDFVPLHYNLYNA 300
QY 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNNDMRNIFNGTVVQRHPSHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTITRE 360

QY 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
QY 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 8
US-10-477-725-13
; Sequence 13, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus 707
US-10-477-725-13

Query Match 100.0%; Score 2703; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.8e-241;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
QY 61 YDYLDFEFNKGTVRTKYGTRSQQAATSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDFEFNKGTVRTKYGTRSQQAATSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQVETGEYITTEAWTRDFPGRGNTSHSFKWRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQVETGEYITTEAWTRDFPGRGNTSHSFKWRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMTADIMDHPVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMTADIMDHPVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
QY 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420

Db 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485

RESULT 9
US-09-854-346-12
; Sequence 12, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-854-346-12

Query Match 96.7%; Score 2613; DB 9; Length 485;
Best Local Similarity 95.5%; Pred. No. 8.2e-233;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKASQNDVGGA 60
QY 61 YDYLDFEFNKGTVRTKYGTRSQQAATSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDYLDFEFNKGTVRTKYGTRSQQAATSLKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQVETGEYITTEAWTRDFPGRGNTSHSFKWRWYHFDGVDWDQSRRLNNRIYKF 180
Db 121 EVNPNRNQVETGEYITTEAWTRDFPGRGNTSHSFKWRWYHFDGVDWDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTEGNGYDYLMTADIMDHPVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDYLMTADIMDHPVNVNELRNWGVWYTNLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLOKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGNYDMRNIENGTVVQRHPSHAVTFVDNHDSDQPEALESFVEEFKPLAYALTITRE 360
QY 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
Db 361 QGYPSVFYGYGIPTHGVPMARSKIDPILFARQKAYGKQNDYLDHNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFWGRNKAGQVWSDITGNRTGTVTINADGWGNSVNGGSVS 480
QY 481 IWVWK 485
Db 481 IWVWK 485


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RESULT 10
US-09-918-543-12
; Sequence 12, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kiaerulf, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-918-543-12

Query Match
Best Local Similarity 96.7%; Score 2613; DB 9; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNAKLSNGIQYVGVVNMHKGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNAKLSNGIQYVGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVVDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVVDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVNVNLRNWGYVNTLGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVNVNLRNWGYVNTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKMFVAFVFNKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSATGKMFVAFVFNKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIENGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRNIENGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFGDYGIPTGTHGVPMKSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFGDYGIPTGTHGVPMKSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKGQVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKGQVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
QY 481 IWVKN 485
DB 481 IWVKN 485

RESULT 11
US-09-925-576C-12
; Sequence 12, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 5276.400-US
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24

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; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-925-576C-12

Query Match
Best Local Similarity 96.7%; Score 2613; DB 10; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNNRLNSDASNLKSKGITAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNAKLSNGIQYVGVVNMHKGADATEMVRV 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNAKLSNGIQYVGVVNMHKGADATEMVRV 120
QY 121 EVNPNRNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVVDQSRRLNNRIYKF 180
DB 121 EVNPNRNOEVTGEYTIETATWTRDFPGRGNTHSSFKRWYHFDGVVDQSRRLNNRIYKF 180
QY 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVNVNLRNWGYVNTLGLDGFRIIDAVKH 240
DB 181 RGHGKAWDEVDTENGNYDLYMADIDMDHPVNVNLRNWGYVNTLGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKMFVAFVFNKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSATGKMFVAFVFNKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRNIENGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRNIENGTVVQRHPHSHAVTFVDNHDQPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFGDYGIPTGTHGVPMKSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFGDYGIPTGTHGVPMKSKIDPILAEARQKAYGKQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGSKMFWGRNKGQVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGSKMFWGRNKGQVWSDITGNRTGTVTINADGNGNFSVNGGSVS 480
QY 481 IWVKN 485
DB 481 IWVKN 485

RESULT 12
US-10-327-837-24
; Sequence 24, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24

```



```
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match
Best Local Similarity 96.7%; Score 2613; DB 12; Length 485;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVIAPPKAWGASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGISAVIAPPKAWGASQNDVGGA 60
Qy 61 YDLYDLGEFNGKQGVTRTKYGTTRSLQAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKQGVTRTKYGTTRSLQAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNOEVTGEYTTIEATWTRPDPGRGNTHSSFKRWYHFDGVDWQSRLLNRIYKF 180
Db 121 EVNPNRNOEVTGEYTTIEATWTRPDPGRGNTHSSFKRWYHFDGVDWQSRLLNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Qy 301 SKSGNVDNRINFGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGNVDNRINFGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPVSFVGYDYGIPTHGVPAKRSKIDPILKARQYAYGKNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVSFVGYDYGIPTHGVPAKRSKIDPILKARQYAYGKNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Qy 481 IWVK 485
Db 481 IWVK 485

RESULT 14
US-10-209-812-5
; Sequence 5, Application US/10209812
; Publication No. US2003008785A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Ostern, Claus von der
; APPLICANT: Andersen, Kim Vilbourn
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/10/209,812
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/417,359
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-209-812-5

Query Match
96.7%; Score 2613; DB 14; Length 485;
```

```
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match
Best Local Similarity 95.5%; Pred. No. 8.2e-233;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVIAPPKAWGASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGISAVIAPPKAWGASQNDVGGA 60
Qy 61 YDLYDLGEFNGKQGVTRTKYGTTRSLQAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKQGVTRTKYGTTRSLQAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNOEVTGEYTTIEATWTRPDPGRGNTHSSFKRWYHFDGVDWQSRLLNRIYKF 180
Db 121 EVNPNRNOEVTGEYTTIEATWTRPDPGRGNTHSSFKRWYHFDGVDWQSRLLNRIYKF 180
Qy 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGHGKAWDEVDTEGNGYDILMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLOKTNWNHVSFVDFVPLHYNLYNA 300
Qy 301 SKSGNVDNRINFGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
Db 301 SKSGNVDNRINFGTVVQRHPSHAVTFVNDHDSQPEEALSFVEEFKPLAYALTITRE 360
Qy 361 QGYPVSFVGYDYGIPTHGVPAKRSKIDPILKARQYAYGKNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPVSFVGYDYGIPTHGVPAKRSKIDPILKARQYAYGKNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVMSDITGNRTGTVTINADGWGNFSVNGGSVS 480
Qy 481 IWVK 485
Db 481 IWVK 485

RESULT 13
US-10-327-837-26
; Sequence 26, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Oustrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-26

Query Match
96.7%; Score 2613; DB 12; Length 485;
```

Best Local Similarity 95.5%; Pred. No. 8.2e-233; Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
Qy	1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKGASQNDVGCGA 60
Db	1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKGASQNDVGCGA 60
Qy	61 YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db	61 YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy	121 EVNPNRNQEVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Db	121 EVNPNRNQEVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKF 180
Qy	181 RHGKAWDEWDTENGNDYLYMADI DMDHPVNVNELRNWGVYNTLGLDGFRI DAVKH 240
Db	181 RHGKAWDEWDTENGNDYLYMADI DMDHPVNVNELRNWGVYNTLGLDGFRI DAVKH 240
Qy	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
Db	241 IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGA IENYLQKTNNHNSVFDVPLHYNLYNA 300
Qy	301 SKSGGNYDMRNIFNGTIVVQRHPHSHAVTFVDNHD SQPEEALSFVBWFKPLAYALTLTRE 360
Db	301 SKSGGNYDMRNIFNGTIVVQRHPHSHAVTFVDNHD SQPEEALSFVBWFKPLAYALTLTRE 360
Qy	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPIL EARKQYAYGKONDYLDHNNIIGWTRRGNTA 420
Db	361 QGYPSVFGDYIGIPTHGVPAMRSKIDPIL EARKQYAYGKONDYLDHNNIIGWTRRGNTA 420
Qy	421 HPNSGLATIMSDGAGGSKMFWGRNKAGOVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Db	421 HPNSGLATIMSDGAGGSKMFWGRNKAGOVWSDITGNRTGTVTINADGWNFSVNGGSYS 480
Qy	481 IWVWK 485
Db	481 IWVWK 485
Search completed: October 7, 2004, 00:57:33 Job time : 54.4478 secs	

Query Match 96.7%; Score 2613; DB 16; Length 485; Best Local Similarity 95.5%; Pred. No. 8.2e-233; Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;	
Qy	1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKGASQNDVGCGA 60
Db	1 HHNGTGTMMQYFEWYLPNDGNHNRLNSDASNLKSGITAVWIPPAWKGASQNDVGCGA 60
Qy	61 YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120
Db	61 YDLYDLGEFNQKGTVRTKYGTRSQLOAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV 120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-13
Perfect score: 2703
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWGNFVNGSGSVSIWNK 485

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2410	89.2	516	2	O82839
2	1947	72.0	533	2	O82839
3	1941	71.8	513	16	O81734
4	1929	71.4	513	16	O81734
5	1888.5	69.9	613	2	O59222
6	1878	69.5	519	2	O90778
7	1876.5	69.4	549	2	O31193
8	1871.5	69.2	521	2	P71034
9	1871.5	69.2	549	2	O9KW6
10	1802.5	66.7	501	2	O93148
11	1570.5	58.1	507	16	O87HG6
12	1360	50.3	493	2	O31657
13	1339	49.5	481	16	O89YF1
14	1280.5	47.7	488	16	O8EOM2
15	1287.5	47.6	486	16	O8D708
16	1283.5	47.5	488	16	O8E696

17	1280	47.4	484	16	Q97Q49
18	1278	47.3	484	16	O8DPC8
19	1275	47.2	492	16	O8YU21
20	1259.5	46.6	486	2	O68875
21	1250.5	46.3	484	2	O50583
22	1246.5	46.1	485	2	O53786
23	1139	42.1	491	16	O9C859
24	1125	41.6	506	16	O8U916
25	1064	39.4	494	16	O8Z555
26	1054	39.0	495	16	O8XBB6
27	1050	38.8	495	16	O8FGL8
28	1043	38.6	495	16	O7UAB0
29	1041	38.5	495	16	O83R40
30	1033.5	38.2	529	3	O877B1
31	474.5	17.6	461	1	O33476
32	474.5	17.6	461	1	O8NKR4
33	459	17.0	469	1	O50200
34	456	16.9	432	14	O8JZK3
35	453.5	16.8	461	1	O8NKR5
36	450.5	16.7	460	1	O9P9L0
37	450.5	16.7	460	1	O08452
38	450.5	16.7	473	17	O8U319
39	442	16.4	457	1	O93647
40	311.5	11.5	482	2	O60051
41	285	10.5	504	1	O60224
42	281.5	10.4	421	10	O7X9T1
43	280	10.4	420	10	O9ZP43
44	279.5	10.3	906	10	O8LQK4
45	279	10.3	424	10	O8LP27

ALIGNMENTS

RESULT 1

O82839 ID O82839 PRELIMINARY; PRT; 516 AA.
AC O82839;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A..
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igaraashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377(1998).
DR EMBL; AB008763; BAA32431.1; -;
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 89.2%; Score 2410; DB 2; Length 516;

Best Local Similarity 86.4%; Pred. No. 6.2e-146;

Matches 419; Conservative 36; Mismatches 30; Indels 0; Gaps 0;

Qy 1 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGA 60

Db 32 HHNGTNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKGTQNDVGYGA 91

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QY 61 YDLYDLGEFNQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRVAV 120
DB 92 YDLYDLGEFNQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRVAV 151
QY 121 EVNPNRNQEVTTIEATWTRDFPGRGNTHSSFKRWYHFPGVDWDQSRRLNNRIYKF 180
DB 152 EVNPNRNQEVTTIEATWTRDFPGRGNTHSSFKRWYHFPGVDWDQSRRLNNRIYKF 211
QY 181 RHGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRWGWYTTNLGLDGRIDAVKH 240
DB 212 RGTGKAWDEVDTEGNGYDLYMADIDMDHPEVNVNLRWGWYTTNLGLDGRIDAVKH 271
QY 241 IKYSFTRDWLNHVRSAVKMFAVAEFKNDLGAENYLOKTNWHSVFDVPLHYNLXNA 300
DB 272 IKYSFTRDWLNHVRSAVKMFAVAEFKNDLGAENYLOKTNWHSVFDVPLHYNLXNA 331
QY 301 SKSGGNYDMRNIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEFKPLAYALTITRE 360
DB 332 SNSSGYFDMRNILNGSVVQKHPTHAFTVDNHDSPQPEALESFVQSWFKPLAYALTITRE 391
QY 361 QGYPSVPGYDYGIPTHGVPMESKIDPILFARQKYAGKQNDYLDHNNIIGWTRGNTA 420
DB 392 QGYPSVPGYDYGIPTHGVPMESKIDPILFARQKYAGKQNDYLDHNNIIGWTRGNTA 451
QY 421 HPNSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFGSVGSVS 480
DB 452 HPNSGLATIMSDGPGGNKMYVGRKAGQVWRDITGNRTGTVTINADGWNFGSVGSVS 511
QY 481 IWYVK 485
DB 512 VVVKQ 516

RESULT 2
Q9AQ54 PRELIMINARY; PRT; 533 AA.
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSP; P06278; 1VUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;
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Query Match 72.0%; Score 1947; DB 2; Length 533;
Best Local Similarity 69.4%; Pred. No. 2.4e-116;
Matches 335; Conservative 62; Mismatches 82; Indels 4; Gaps 2;

QY 6 NGTMQYFEWYLPNDGNHNLRLSDASNLKSGITAYVIPPWKASQNDVGAYDLYD 65
DB 52 NGTMQYFEWYLPNDGNHNLRLSDAENLAKGITSVWIPFAYKGTQNDVGAYDLYD 111
QY 66 LGFENQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRVAVPN 125
DB 112 LGFENQKGTVRTKYGTRSOLOAAVTSLNKNGIQVYGDVVMNHKGGADATEMVRVAVPN 171
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QY 126 NRNQEVTGTYTIEATWTRDFPGRGNTHSSFKRWYHFPGVDWDQSRRLNNRIYKFRGHGK 185
DB 172 NRNVEVSGDYELISAWTGFNFGPGRGDSYSNFKWKYHFDGTDWDEGRKL-NRIYKFRGIGK 230
QY 186 AMDWEVDTEGNGYDLYMADIDMDHPEVNVNLRWGWYTTNLGLDGRIDAVKHICYSF 245
DB 231 AMDWEVSSGNGYDLYMADIDMDHPEVNVNLRWGWYTTNLGLDGRIDAVKHIDHEY 290
QY 246 TRDWNHVSATGKMFVAEFAEKNDLGAENYLOKTNWHSVFDVPLHYNLNASKSGG 305
DB 291 LRDNVNHVQQTKEMFAVAEYQNDIQTLNNYLAKVNTNSQVDFDPLHNYHYASKNG 350
QY 306 NYDMRNIFNGTVVQRHPSHAVTFVDNHDSPQPEALESFVEEFKPLAYALTITREOGYPS 365
DB 351 NYDMRNILKGTVVVNHPTLAVTLVENHDSQPQGSLESVVSFWFKPLAYAFILTRABGYPS 410
QY 366 VFYGDYIGI---PTHGVPAMRSKIDPILFARQKYAGKQNDYLDHNNIIGWTRGNTAHP 422
DB 411 VFYGDYIGI---PTHGVPAMRSKIDPILFARQKYAGKQNDYLDHNNIIGWTRGNTAHP 470
QY 423 NSGLATIMSDGAGGSKMFMVGRNKAGQVWSDITGNRTGTVTINADGWNFGSVGSVS 482
DB 471 NSGLATIMSDGPGGNKMYVGRKAGQVWRDITGNRTGTVTINADGWNFGSVGSVS 530
QY 483 VNK 485
DB 531 VQR 533

RESULT 3
Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Riststone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.P.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423.81-86(2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_aml_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;
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Query Match 71.8%; Score 1941; DB 16; Length 513;
Best Local Similarity 69.4%; Pred. No. 5.6e-116;
Matches 335; Conservative 63; Mismatches 81; Indels 4; Gaps 2;
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QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYD 65
 DB 32 NGTLMQYFEWYAPSDRHNHNRRLRTDAENLAQKSGITSVIPPAWKGTQNDVGYGAYDLYD 91
 QY 66 LGFENQKGTVRTKYGTSQLOAAVTSLKNGIQYQYGVDMVNMHKGADATEMVRVAVENPN 125
 DB 92 LGFENQKGTVRTKYGTSQLOAAVTSLKNGIQYQYGVDMVNMHKGADATEMVRVAVENPN 151
 QY 126 NRQOEVTEGYTIEAWTRFDPGRGNTHSSFKRWYHFDGVDWDSRRLNRIYKFRGHGK 185
 DB 152 NRNVESGDYEISAWTGFNPGRGDYSNFKRWYHFDGVDWDSRRLNRIYKFRGHGK 210
 QY 186 AWDWEVDTENGNDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIXYSF 245
 DB 211 AWDWEVSENGNDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIDHEY 270
 QY 246 TRDWINHVRSGATGKMFPAVEFKNLGAENYILQKTNMHSVDFDPLHYNLYNASKSGG 305
 DB 271 LRDMVNHVRQGTGKMFPAVEFKNLGAENYILQKTNMHSVDFDPLHYNLYNASKSGG 330
 QY 306 NYDMRNIFNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGVPS 365
 DB 331 NYDMRNILNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGVPS 390
 QY 366 VFYGDYVGI---PTHGVPAMRSKIDPILKARQYAYKQNDYLDHNNIIGWTRGNTAHP 422
 DB 391 VFYGDYVGI---PTHGVPAMRSKIDPILKARQYAYKQNDYLDHNNIIGWTRGNTAHP 450
 QY 423 NSGLATIMSDGAGSKMVFGRNKGQVMSDITGNRTGTTINADGNFVSGSVSIW 482
 DB 451 NSGLATIMSDGAGSKMVFGRNKGQVMSDITGNRTGTTINADGNFVSGSVSIW 510
 QY 483 VNK 485
 DB 511 VQO 513

RESULT 4

Q81A54 PRELIMINARY; PRT; 513 AA.
 AC Q81A54;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DE Glucan 1,4-alpha-maltohexaoidase (EC 3.2.1.98).
 GN BC3482.
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608415; PubMed=12721630;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 Kapural V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
 Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
 Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 Overbeek R., Kyrpides N.,
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis";
 RL Nature 423:87-91(2003).
 DR EMBL; AE017009; AAP10417.1; --
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase; Complete proteome.
 SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BF9F9F6 CRC64;

Query Match

71.4%; Score 1929; DB 16; Length 513;

Best Local Similarity 68.7%; Pred. No. 3.3e-115;
 Matches 332; Conservative 62; Mismatches 85; Indels 4; Gaps 2;
 QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVWIPPAWKASQNDVGYGAYDLYD 65
 DB 32 NGTLMQYFEWYAPSDRHNHNRRLRTDAENLAQKSGITSVIPPAWKGTQNDVGYGAYDLYD 91
 QY 66 LGFENQKGTVRTKYGTSQLOAAVTSLKNGIQYQYGVDMVNMHKGADATEMVRVAVENPN 125
 DB 92 LGFENQKGTVRTKYGTSQLOAAVTSLKNGIQYQYGVDMVNMHKGADATEMVRVAVENPN 151
 QY 126 NRQOEVTEGYTIEAWTRFDPGRGNTHSSFKRWYHFDGVDWDSRRLNRIYKFRGHGK 185
 DB 152 NRNVESGDYEISAWTGFNPGRGDYSNFKRWYHFDGVDWDSRRLNRIYKFRGHGK 210
 QY 186 AWDWEVDTENGNDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIXYSF 245
 DB 211 AWDWEVSENGNDYLMYADIDMDHPEVNMELRWNGVYNTLGLDGFRIIDAVKHIDHEY 270
 QY 246 TRDWINHVRSGATGKMFPAVEFKNLGAENYILQKTNMHSVDFDPLHYNLYNASKSGG 305
 DB 271 LRDMVNHVRQGTGKMFPAVEFKNLGAENYILQKTNMHSVDFDPLHYNLYNASKSGG 330
 QY 306 NYDMRNIFNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGVPS 365
 DB 331 NYDMRNILNGTVQORHPSHVAFTVDNHDSPQEALESFVEWFKPLAYALTLTREOGVPS 390
 QY 366 VFYGDYVGI---PTHGVPAMRSKIDPILKARQYAYKQNDYLDHNNIIGWTRGNTAHP 422
 DB 391 VFYGDYVGI---PTHGVPAMRSKIDPILKARQYAYKQNDYLDHNNIIGWTRGNTAHP 450
 QY 423 NSGLATIMSDGAGSKMVFGRNKGQVMSDITGNRTGTTINADGNFVSGSVSIW 482
 DB 451 NSGLATIMSDGAGSKMVFGRNKGQVMSDITGNRTGTTINADGNFVSGSVSIW 510
 QY 483 VNK 485
 DB 511 VQO 513

RESULT 5
 Q59222 PRELIMINARY; PRT; 613 AA.
 AC Q59222;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha-amylase (EC 3.2.2.1).
 GN AMY.
 OS Bacillus sp. TS-23.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=38441;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=TS-23;
 RA Lin L.-L., Chu W.S., Hsu W.H.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U22045; AAA63900.1; --
 DR HSP; P06278; IVS.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha_amyl_cat.
 DR InterPro; IPR006589; Alp_amyl_cat_sub.
 DR InterPro; IPR002044; CBD_4.
 DR Pfam; PF00128; alpha-amylase; 13.
 DR Pfam; PF006046; Glyco_hydro_1.
 DR PRINTS; PR00110; ALPHAAMYLASE.
 DR ProDom; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 KW Glycosidase; Hydrolase.

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SQ SEQUENCE 613 AA; 69537 MW; 14694A30FC2895E8 CRC64;
Query Match 69.9%; Score 1888.5; DB 2; Length 613;
Best Local Similarity 68.1%; Pred. No. 1.6e-112;
Matches 327; Conservative 66; Mismatches 86; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 65
DB 36 NETMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 95

QY 66 LGBFNQKGTVRTKYGTRSQLQAAYTSLKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 125
DB 96 LGBFNQKGTVRTKYGTRSQLQAAYTSLKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 155

QY 126 NRNOEVTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 185
DB 156 NRNOEVTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 214

QY 186 AWDWEVDVTENGNDYLMYADIDMDHPEVNVNLRNWGYVYTNLTGLDGFRIIDAVKHIKYSF 245
DB 215 AWDWEVDVTENGNDYLMYADIDMDHPEVNVNLRNWGYVYTNLTGLDGFRIIDAVKHIKYSF 274

QY 246 TRDWINHRSATGKNMFVAFVFNKDLGALNIYKQTNWHSVDPVPLHLYNLYNASKSG 305
DB 275 FPDWLTAVRNQTKNLFVAGFEFWSYDNKLNHTITKNGSMFLDAPLHNNFYTASKSG 334

QY 306 NYDMRNIFNGTVVQRHPSHAFTVDNHDSDPEEALSFVEWFKPLAYALTLTREOGYPS 365
DB 335 YFDMRYLNNLTWKDQPSLAVTLVDNHDTPGQSLQSWEPFKPLAYAFILTRQGYPC 394

QY 366 VFYGDYGGIPTHGVPMRSKIDPILKARQYKAYGKQNDYLDHNNIIGWTRGNTAHPSNG 425
DB 395 VFYGDYGGIPKYNIPGLKSKIDPLLTARDYAYGTQRDYIDHQDIIGWTRGNTAHPSNG 454

QY 426 LATIMSDGAGSKMFGVGRNKGQVWSDITGNRTGTVTINADGWFNSVNGSGSVIWNK 485
DB 455 LAALITDPGSGKMYVGGKHAGKFYFDLTGNRSDTVTINADGWFNSVNGSGSVIWNK 514

RESULT 6
ID Q9ROT8 PRELIMINARY; PRT; 519 AA.
AC Q9ROT8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Raw search digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
OC Flexibacteraceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF00567.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 519 AA; 58337 MW; 3B6B88A4DF98B163 CRC64;
Query Match 69.5%; Score 1878; DB 2; Length 519;
Best Local Similarity 67.4%; Pred. No. 6e-112;
Matches 326; Conservative 71; Mismatches 83; Indels 4; Gaps 2;

QY 5 TNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLY 64
DB 37 TNGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLY 96

QY 65 DLGEFNQKGTVRTKYGTRSQLQAAYTSLKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 124
DB 97 DLGEFNQKGTVRTKYGTRSQLQAAYTSLKNGIQYVGDVVMNHKGGADATAMVRAVEVNP 156

QY 125 NRNOEVTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 184
DB 157 NRNOEVTGEYTIETAWTRFDFPGRGNTHSSFKRWYHFDGVDWDQSRRLNNRIYKFRGHG 215

QY 185 KAWDWEVDVTENGNDYLMYADIDMDHPEVNVNLRNWGYVYTNLTGLDGFRIIDAVKHIKYS 244
DB 216 KAWDWEVDVTENGNDYLMYADIDMDHPEVNVNLRNWGYVYTNLTGLDGFRIIDAVKHIKYS 275

QY 245 FTRDWINHRSATGKNMFVAFVFNKDLGALNIYKQTNWHSVDPVPLHLYNLYNASKSG 304
DB 276 FLKDWVDNARAATGKEMFTVGEYQNDLGLALNNYLAQVNYNQSFLDAPLHNYFYAASG 335

QY 305 GNYDMRNIFNGTVVQRHPSHAFTVDNHDSDPEEALSFVEWFKPLAYALTLTREOGYPS 364
DB 336 GNYDMRNILNLTVASNPTKAVTLVDNHDTPGQSLQSWEPFKPLAYAFILTRSGGYP 395

QY 365 SVFYGDY--GIPTHGVPMRSKIDPILKARQYKAYGKQNDYLDHNNIIGWTRGNTAH 421
DB 396 SVFYGDYMGTKGTTREIPALSKIEPLKARKDQYAYGTQRDYIDNPVIGWTRGDSYK 455

QY 422 PMSGLATIMSDGAGSKMFGVGRNKGQVWSDITGNRTGTVTINADGWFNSVNGSGSVI 481
DB 456 AKSGLATVITDPGSGSKMYVGTSGNAGEIWDLTGNRTKTIIGSDGYATFPVNGSGSV 515

QY 482 WYNNK 485
DB 516 WYQQ 519

RESULT 7
ID Q31193 PRELIMINARY; PRT; 549 AA.
AC Q31193
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha amylase.
OS AMI.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 31195;
RA da Silva A.C.R., Fernandes E., Pueyo M.T.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF032864; AAB86961.1; -.
DR PIR; A54541; A54541.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 549 AA; 62651 MW; 2CA689BDACC4D262 CRC64;
Query Match 69.4%; Score 1876.5; DB 2; Length 549;
Best Local Similarity 67.4%; Pred. No. 8e-112;
Matches 322; Conservative 75; Mismatches 80; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGAYDLYD 65
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Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITATLWLPAYKGTSRSDVGYGYDLYD 98
Qy 66 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 158
Qy 126 NRNEQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKPRGHGK 185
Db 159 DRNQEISGTYQIQAWTKFDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKPRGHGK 217
Qy 186 AWDMEVDTEGNGYDLYMADIMDHPPEVNNELRWNGVWYTTNLGLDGRIDAVKHIKYSF 245
Db 218 AWDMEVDTEGNGYDLYMADIMDHPPEVNNELRWNGVWYTTNLGLDGRIDAVKHIKYSF 277
Qy 246 TRDWINHVSATGKMFVAEFAWKNLGLGAIENYLOKTNWHSVDFVPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTKPLFTVGEYWSYDINKLHNYITKNGTMSLFDAPLHNKFYTASKSGG 337
Qy 306 NYDMRNFTNGTVQVRHPSHATVFDNHDSPQEEALESFVEEWFKPLAYALTITREOGYPS 365
Db 338 AFDNRTLTMTNLMKDQPTLAVTFVDNHDTEPQALQSWVDPWFKPLAYALTITREOGYPS 397
Qy 366 VFYGDYGIPTGHPVPMRSKIDPILFARQKAYQKNDYLDHNNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHPVPMRSKIDPILFARQKAYQKNDYLDHNNIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGSKWFMVGRNKGAGVMSDITGNRTGTVTINADGNGFVNGSGSVSIW 483
Db 458 LAALITDGPGGSKWMTYGVKQHAGKVFYDLTGNRSDTVTINSDGNGFVNGSGSVSIW 515

RESULT 8
P71034
ID AC P71034 PRELIMINARY; PRT; 521 AA.
AC Q9KMY6;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase precursor.
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
RL thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 521 AA; 59311 MW; 5612A88596D922E1 CRC64;

Query Match 69.2%; Score 1871.5; DB 2; Length 521;
Best Local Similarity 67.2%; Pred. No. 1.6e-111;
Matches 321; Conservative 75; Mismatches 81; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITATLWLPAYKGTSRSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITATLWLPAYKGTSRSDVGYGYDLYD 98
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Qy 66 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 158
Qy 126 NRNEQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKPRGHGK 185
Db 159 DRNQEISGTYQIQAWTKFDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKPRGHGK 217
Qy 186 AWDMEVDTEGNGYDLYMADIMDHPPEVNNELRWNGVWYTTNLGLDGRIDAVKHIKYSF 245
Db 218 AWDMEVDTEGNGYDLYMADIMDHPPEVNNELRWNGVWYTTNLGLDGRIDAVKHIKYSF 277
Qy 246 TRDWINHVSATGKMFVAEFAWKNLGLGAIENYLOKTNWHSVDFVPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTKPLFTVGEYWSYDINKLHNYITKNGTMSLFDAPLHNKFYTASKSGG 337
Qy 306 NYDMRNFTNGTVQVRHPSHATVFDNHDSPQEEALESFVEEWFKPLAYALTITREOGYPS 365
Db 338 AFDNRTLTMTNLMKDQPTLAVTFVDNHDTEPQALQSWVDPWFKPLAYALTITREOGYPS 397
Qy 366 VFYGDYGIPTGHPVPMRSKIDPILFARQKAYQKNDYLDHNNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHPVPMRSKIDPILFARQKAYQKNDYLDHNNIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGSKWFMVGRNKGAGVMSDITGNRTGTVTINADGNGFVNGSGSVSIW 483
Db 458 LAALITDGPGGSKWMTYGVKQHAGKVFYDLTGNRSDTVTINSDGNGFVNGSGSVSIW 515

RESULT 9
Q9KMY6
ID AC Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Bejar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B66DF9120BCE CRC64;

Query Match 69.2%; Score 1871.5; DB 2; Length 549;
Best Local Similarity 67.2%; Pred. No. 1.7e-111;
Matches 321; Conservative 75; Mismatches 81; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITATLWLPAYKGTSRSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLSSLGITATLWLPAYKGTSRSDVGYGYDLYD 98
Qy 66 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTSRQLOAAVTSLKNGIQVYGVYVMMHKGADATMVRVAVENPN 158
Qy 126 NRNEQVTEGYTIEAWTRDFPGRGNTHSSFKRWYHFDGVWDQSRRLNNRIYKPRGHGK 185
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Db 322 SGNNDMEQIMNGTLKMKONPVKAVTLNENHDTQPLQALESTVDWMFKPLAYAFILLRBEQ 381
Qy 363 YPSVFGDYGG-----IPTHGVPMARSKIDPILARQKYAYGKQNDYLDHNIIGW 413
Db 382 YPSVYADYGAQYSDKGNINMAKVP-----YIELVTLRKEYAYGKQNSYLDHWDVLGW 437
Qy 414 TREGTAHPNSGLATIMSDGAGSKMFMVGRNKAGQVMSDITGNRTGTTINADGWNFS 473
Db 438 TREGDAEPNS-MAVIMSDGPGTKMYTKPSTRYV--DKLGIREEVWTDANGWAEFP 494
Qy 474 VNGGSVSIWV 483
Db 495 VNGGSVSVWV 504

RESULT 12
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; PRCDD2F805BB4694 CRC64;

Query Match 50.3%; Score 1360; DB 2; Length 493;
Best Local Similarity 50.9%; Pred. No. 5.9e-79;
Matches 245; Conservative 78; Mismatches 150; Indels 8; Gaps 3;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVMIPPAMKASQNDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAADGDHMKELAEMAPLAKAGIDTVWVPVTKAVSAEDTGYGYDLYD 63

Qy 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATEMVRVAVNPN 125
Db 64 LGFEDQKGTVRTKYGTSQLOELIAEACQKNGIAVVDLVNMHKGADATEMVRVAVNPN 123

Qy 126 NRNEQVTEGYTIEAWTRDFPGRGNTHSSFKWRNYHFDGVDWDQSRRLNRIYKFRGHGK 185
Db 124 DRTKEISPEPFEIGWTFTFPGRGDQVSSFKWNEHFNGTDFD-AREERTGVFPIAGENK 182

Qy 186 AWDMEVTENGNYDYLMAVDIMDHPVNMELRWNVYNTLTGLDGRIDAVKHICYSF 245
Db 183 KWNENVDDEFGNYDYLMAFNIDYNHDPVVRMIDWKGWLIDTLQCGGFRIDAIKHINHEF 242

Qy 246 TRDWINHVRATGKMFVAFEFKWNLDGAIENYLOKTNWNHNSVDFVPLHYNLYNASKSGG 305
Db 243 IKEFAAEIMRKRGQDFYVIGSFNNSLDACREFLDTVYQIDLDLFDVSLHYKLHEASLGR 302

Qy 306 NYDMRNTFNGTVQRHPSHAVTFVDNHDSPHEALESFVEWFKPLAYALTLTREQQYPS 365
Db 303 DFDLSKIFDDTLVQTHPTAVTFVDNHDSPHEALESIGWIDWFKPSPAYALTLLRRDGYPV 362

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Qy 366 VFYGDYGI-----PTHGVPMARSKIDPILARQKYAYGKQNDYLDHNIIGWTRGNTAH 421
Db 363 VFYGDYGI-----KKEILDILLSARCNKAYGEQEDYFDHANTIGWVRGVERI 419
Qy 422 PNSGLATIMSDGAGSKMFMVGRNKAGQVMSDITGNRTGTTINADGWNFSVNGGSVSI 481
Db 420 EGSQCAVVISNGDGEKRMFIEGHRAGEVWVDLTKSCDDQITIEEDGWATPHVCGGVS 479
Qy 482 W 482
Db 480 W 480

RESULT 13
Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 49.5%; Score 1339; DB 16; Length 481;
Best Local Similarity 49.8%; Pred. No. 1.5e-77;
Matches 239; Conservative 86; Mismatches 153; Indels 2; Gaps 2;

Qy 6 NGTMMQYFEWYLPNDGNHNRNLNSDASNLKSGITAVMIPPAMKASQNDVGYGAYDLYD 65
Db 3 NGVMMQYFEWHLPNDKLWKQIKEDALHLHDIGTAVMIPPAYKADQDEGYATYDLYD 62

Qy 66 LGFENQKGTVRTKYGTSQLOAAVTSLNKNGIQYGVDMVNMHKGADATEMVRVAVNPN 125
Db 63 LGFEDQKGTVRTKYGTSQDELKMDLKHVIAVVDLVNMHKGAGDTEKFMVVEVDPK 122

Qy 126 NRNEQVTEGYTIEAWTRDFPGRGNTHSSFKWRNYHFDGVDWDQSRRLNRIYKFRGHGK 185
Db 123 ERTKALGEPFEIQGTGYSGHGRKDKHSDFKWYHFSGTGTFDDAQK-RSGVFQIQSGEK 181

Qy 186 AWDMEVTENGNYDYLMAVDIMDHPVNMELRWNVYNTLTGLDGRIDAVKHICYSF 245
Db 182 AWSGVDSENGNYDFLNCNDLIDLPVPSLNKRWKWSNELMDGRLDAIKHMKDQF 241

Qy 246 TRDWINHVRATGKMFVAFEFKWNLDGAIENYLOKTNWNHNSVDFVPLHYNLYNASKSGG 305
Db 242 VAQFLDAVRSEKGNDFYAVGVWNGDLEALDAYIEAVGHKYNLFDVPLHYNMFOASQEGK 301

Qy 306 NYDMRNTFNGTVQRHPSHAVTFVDNHDSPHEALESFVEWFKPLAYALTLTREQQYPS 365
Db 302 DYDLRLDKDTLVHEHPDLAVTIVDNHDTQRGSSLESNVEDWFKPLAYGLTLLMKEGYPC 361
Qy 366 VFYGDYGIPTHGVPMARSKIDPILARQKYAYGKQNDYLDHNIIGWTRGNTAHPSNG 425

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362 LFYGDYVIGKEKSPHTRI-IDILLDARRKAYAGDQIEVFDHPSTGTFIRTDGDEHNGSG 420
426 LATIMSDGAGGSKWFMFVGRNKAGQVMSDITNGRTGTVTINADGWNFSVNGGVSIVWVK 485
421 LVFIMSNDEAGSKIMSLGKHKGEVWHEITGSISSBEITLDEEGNGEFSVESRLNAVWVK 480

RESULT 14
Q8E0M2 PRELIMINARY; PRT; 488 AA.
AC Q8E0M2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eissen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Ken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AE014223; AAM99595.1; -.
DR TIGR; SAG0708; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR InterPro; IPR006046; Glyco hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 47.7%; Score 1290.5; DB 16; Length 488;
Best Local Similarity 48.8%; Pred. No. 1.9e-74;
Matches 23; Conservative 82; Mismatches 158; Indels 9; Gaps 5;

QY 5 TNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGVDLY 64
DB 2 TNELIMQAFEWYLPDSDGNHKKLBEESLDLKLGIKIMLPAPKGTSSDDVGYGYDLF 61
QY 65 DLGEFNQKGTVRTKYGTRSQLQAAYVTSLKNGIQVYGDVVMNHKGADATEMVRVAVNP 124
DB 62 DLGEFDQNGTIRTKYGRKEEYLKLIKSLKANGIKPFADIVLNHKGADHKEKFOVKNP 121
QY 125 NNRNOEVTGYTTEAWTRFPDPPGRGNTHSSFKRWYHFDGVDWQSRRLNRR--IYKFRG 182
DB 122 ENRQALSEPYEIEGWTGTFDPPGRQGEYNDPKWHYHFTGLDYDAK---NNEITDFIVG 178
QY 183 HGKAW--DWEVDTENGNYDILMYADI DMHDPVNVNELNMGVWYNTLTGLDGRFIDAVKH 240
DB 179 DNKGWADDLIDDENGFNFDLYMYNDIDFKGPEVINKLQDWAQWFIETTGIEGFRDLAVKH 238
QY 241 IKYSFTRDWINHVSATGKNMFAVEFKQNDLGAENYLOKTNWNHVSFVDVPLHNYLNA 300
DB 239 IDSIFYIQTFFINDIRTKIKPDLEVFGEYWNKSDQTSNKOYLEATQFQSLVDVTLHWNFFDA 298

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301 SKSGGNYDMRNITFNGTVVORHPSHVAVTVDNHDSDPEEALSFVEWFKPLAYALTLTRE 360
299 SHQRNDFDMRTIFDDSLVIDNPEYAVTFVENHDTSQGALESFVEDWFKPLAYGLILLHQ 358
361 QGYPSVFGDYGIP-THGVPAMRSKIDPILAEAROKYAYGKONDYLDHNIIGWTREGNT 419
359 QGTPLCFYGDYIGOGFQCFKEVIDKMAELRQNYVEGKQVDYFTHSNCIGWTCGLGDE 418
420 AHPNSGLATIMSDGAGGSKWFMFVGRNKAGQVMSDITNGRTGTVTINADGWNFSVNGSV 479
419 EH-NSCLAVVLINGDQGWKMEVGEIYAGKTFVDYLGENCEQEVVIGDDGWDGFLVESASI 477
480 SIWVVK 485
478 SAWVPK 483

RESULT 15
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AE014990; AAN59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1. Complete proteome.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 47.6%; Score 1287.5; DB 16; Length 486;
Best Local Similarity 49.2%; Pred. No. 2.9e-74;
Matches 238; Conservative 72; Mismatches 169; Indels 5; Gaps 4;

QY 5 TNGTMQYFEWYLPNDGNHNRNLNSDASNLKSGKITAVWIPPAWKASQNDVGYGVDLY 64
DB 2 TNETMQYFEWYLPNDGKHWQLAEDASHLKNIGISKVWMPAPKGTGSNDVGYGYVDLY 61
QY 65 DLGEFNQKGTVRTKYGTRSQLQAAYVTSLKNGIQVYGDVVMNHKGADATEMVRVAVNP 124
DB 62 DLGEFNQNGTIRTKYGRSDYLNALKEQELMPSIDIVLNHKGADAKERFOVKNP 121
QY 125 NNRNOEVTGYTTEAWTRFPDPPGRGNTHSSFKRWYHFDGVDWQSRRLNRRNRYKFRGHG 184
DB 122 SNRQEKISEPYEIEGWTGTFDPPGRQGEYNDPKWHYHFTGLDYDALHN-ENGIVMILGDN 180
QY 185 KAW--DWEVDTENGNYDILMYADI DMHDPVNVNELNMGVWYNTLTGLDGRFIDAVKH 242
DB 181 KGWASQENIDQENGNYDILMYDDIDFKGPEVQEHLDWVAFLETSGVGGRFLDAIKHID 240
QY 243 YSTRDWINHVSATGKNMFAVEFKQNDLGAENYLOKTNWNHVSFVDVPLHNYLNASK 302

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Db      241 KTFMAQFIRYIREHLKADLYVFGYWKDSHPDITDYLHSVDLQDFDLIDVMLHMSLFEAGQ 300
Qy      303 SGGNYDMRNI FNGTVQRPSPSHAVTFVDNHDSPPEALESEFVEWFKPLAYALTITREQG 362
Db      301 KGSDFDLSTILDDSLMKSHPDFAVTFVDNHDSPQQALESFVAEFKPLAYGLILLREQG 360
Qy      363 YPSVFGDYGIP-THGVPMRSKIDPILFARQKAYKQNDYLDHNNIIGWTREGNTAH 421
Db      361 IPCVFGDYGYGISGEFAQESFQTVLDKLLYIRQYHVYGSQEDYFDYANCIGWTCIGDBEH 420
Qy      422 PNSGLATIMSDGAGGSKWVFGRNKAGQVMSDITGNRTGTVINADGWGNSVNGGVSU 481
Db      421 PD-GVAVIISNGEANCRRMNGEFNRNKFVDYLNCTEVLDDQGWGDPFVQESLSA 479
Qy      482 WVNK 485
Db      480 WVNK 483

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